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OM protein - protein search, using sw model

Run on: March 28, 2005, 08:33:43 ; Search time 119 Seconds

(without alignments)

34.425 Million cell updates/sec

Title: US-10-036-918B-4**Perfect score:** 33**Sequence:** 1 XPRXRPLX 8**Scoring table:** BL0SUM2

Gapext 10.0 , Gapext 0.5

Searched:

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378**Minimum DB seq length:** 0**Maximum DB seq length:** 200000000**Post-processing:** Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries**Database :** UniProt_03;*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	90.9	269	2	07NFB5
2	30	90.9	285	2	096W33
3	30	90.9	295	2	P95666
4	30	90.9	320	2	Q98K74
5	30	90.9	325	2	08EH66
6	30	90.9	333	2	Q89ML3
7	30	90.9	360	2	Q8UH95
8	30	90.9	460	1	07JPK1
9	30	90.9	540	1	Q9V218
10	30	90.9	569	2	052305
11	30	90.9	877	2	Q23853
12	30	90.9	1100	1	JAK3_RAT
13	29	87.9	157	2	096W24
14	29	87.9	253	2	Q03093
15	29	87.9	257	2	Q7P833
16	29	87.9	312	2	Q9PI62
17	29	87.9	313	2	Q8RG39
18	29	87.9	317	2	Q7VP13
19	29	87.9	315	1	ACCA_HAEIN
20	29	87.9	315	2	Q886W7
21	29	87.9	315	2	Q88GK4
22	29	87.9	316	2	Q9HXZ2
23	29	87.9	317	2	Q7VPL3
24	29	87.9	317	2	Q8D2H6
25	29	87.9	317	2	Q9Cnx9
26	29	87.9	318	1	ACCA_ECOLI
27	29	87.9	318	1	ACCA_SALTY
28	29	87.9	319	2	Q667k5
29	29	87.9	319	2	Q8PAW9
30	29	87.9	319	2	Q8PPM1
31	29	87.9	319	2	Q8ZHS2

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16	29	87.9	312	2	Q9PI62
17	29	87.9	313	2	Q8RG39
18	29	87.9	317	2	Q7VP13
19	29	87.9	315	1	ACCA_HAEIN
20	29	87.9	315	2	Q886W7
21	29	87.9	315	2	Q88GK4
22	29	87.9	316	2	Q9HXZ2
23	29	87.9	317	2	Q7VPL3
24	29	87.9	317	2	Q8D2H6
25	29	87.9	317	2	Q9Cnx9
26	29	87.9	318	1	ACCA_ECOLI
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28	29	87.9	319	2	Q667k5
29	29	87.9	319	2	Q8PAW9
30	29	87.9	319	2	Q8PPM1
31	29	87.9	319	2	Q8ZHS2

ALIGNMENTS

RESULT 1		Best Local Similarity 71.4%; Pred. No. 2.4e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
ID Q7NFB5	PRELIMINARY;	PRT;	269 AA.
ID Q7NFB5;			
AC Q7NFB5;			
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)			
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE G113641; protein.			
GN OrderedlocusName=g113641;			
OS Gloeobacter violaceus.			
OC Bacteria; Cyanobacteria; Chroococcales; Gloeobacter.			
OX NCBI_TAXID=33072;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=PCC 7421;			
RX MEDLINE=22977040; PubMed=14621292;			
RA Nakamura Y., Kameko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,			
RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyohara C.,			
RA Tokuechi C., Yamada M., Tabata S.,			
RT "Complete genome structure of <i>Gloeobacter violaceus</i> PCC 7421, a cyanobacterium that lacks thylakoids.";			
RL DNA Res. 10:137-145 (2003).			
DR EMBL; AP00580; BAC91582.1; -;			
KW Complete proteome.			
SQ SEQUENCE 269 AA; 30697 MW; 67644AFBA107FF2B CRC64;			
Query Match Score 90.9%; DB 2; Length 269; Best Local Similarity 71.4%; Pred. No. 2.3e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY 2 PXRPyXL 8			
Db 186 PARPyTL 192			
RESULT 2		Best Local Similarity 71.4%; Pred. No. 2.4e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
O96WP3	PRELIMINARY;	PRT;	286 AA.
ID O96WP3			
AC O96WP3;			
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT 01-DEC-2004 (TREMBLrel. 26, Last annotation update)			
DE Urease.			
GN Name=URE;			
OS Arthroderra benhamiae (Trichophyton mentagrophytes); Ascomycota; Eurotiomycetes;			
OC Eukaryota; Fungi; Ascomycota; Eurotiomycetes;			
Oxygenales; Arthrodermataceae; Arthroderra.			
OX NCBI_TAXID=63400;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=VUT-77011;			
RA Kano R., Hasegawa A.;			
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
CC -I-CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3)			
CC -I-COFACTOR: Binds 2 nickel ions per subunit (By similarity).			
CC -I-SIMILARITY: Belongs to the urease family.			
DR EMBL; AB069970; BAB62910.1; -.			
DR HSSP; P18314; IEJK.			
DR GO; GO:0016787; F-hydrolase activity; IEA.			
DR GO; GO:0016151; F-nickel ion binding; IEA.			
DR GO; GO:0009059; Fururease activity; IEA.			
DR GO; GO:0006807; P-nitrogen metabolism; IEA.			
DR InterPro; IPRO006680; Amidohydrolase.			
DR InterPro; IPRO005848; Urease_alpha.			
DR Pfam; PF01979; Amidohydro_1; 1.			
DR PRINTS; PR01752; UREASE			
DR PROSITE; PS00145; UREASE_2; 1.			
KW Hydrolase; Metal-binding; Nickel.			
SQ SEQUENCE 286 AA; 31471 MW; AFDD90EA7BCB9A7 CRC64;			
Query Match Score 90.9%; DB 2; Length 286;			

RA Raymond C., Rouse G., Saengphimachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordian-Kamm B., Liao L., Kim C., Hendrickson T., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 CSB.",
 RL Science 294:2317-2323 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cereon;
 RX MIDLINE=2168851; PubMed=11743194; DOI=10.1126/science.1066803;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,
 RA Qurollo B., Goldman B.S., Cao Y., Askew M., Halling C., Mullin L.,
 RA Rounik B., Goldman J.J., Vaudin M., Iartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughy D., Scott C., Lappas C., Marielz B.,
 RA Flanagan C., Crowell C., Gubson J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens CSB.;"
 RL Science 294:2323-2328 (2001).
 DR EMBL; AE009041; AAL41743.1; -.
 DR EMBL; AE008007; ARK86537.1; -.
 DR PTR; H97447; H97447.
 DR HESP; P00216; IE02.
 DR GO; GO:000589; Fe-electron transporter activity; IEA.
 DR GO; GO:0016491; Fe-oxidoreductase activity; IEA.
 DR InterPro; IPR006058; Fe-electron transport; IEA.
 DR InterPro; IPR008333; Fe-binding_6.
 DR InterPro; IPR001041; Ferredoxin.
 DR InterPro; IPR001709; FeN cyt reductse.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR InterPro; IPR001221; Phe_hydroxylase.
 DR Pfam; PF000111; FeZ; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR PRINTS; PR00371; FPNCR.
 DR PRINTS; PR00410; PHENYRLYLASE.
 DR PROSITE; PS00197; 2FE2S_FERREDOXIN_1; Metallo-binding; Complete proteome.
 DR 2FE2S; Iron; Iron-sulfur; Metallo-binding; Complete proteome.
 SQ SEQUENCE 360 AA; 39804 MW; 4EBFP493E850BA0 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 360;
 Best Local Similarity 71.4%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPXPL 8
 Db 77 PSRPyAL 83

RESULT 8

QJPK1 PRELIMINARY; PRT; 460 AA.

ID QJPK1; PRELIMINARY; PRT; 460 AA.

AC QJPK1; PRELIMINARY; PRT; 460 AA.

DT 05-JUL-2004 (TREMBL; 27, Created)
 DT 05-JUL-2004 (TREMBL; 27, Last sequence update)
 DT 05-JUL-2004 (TREMBL; 27, Last annotation update)

DE Hypothetical protein.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 OX NCBI_TaxId=4689;
 RN [1] SEQUENCE FROM N.A.

RC STRAIN=Ax3;
 RX MEDLINE=R_91002566; PubMed=1976383;
 RA Giorda R., Ohmachi T., Shaw D.R., Ennis H.L.,
 RT "A shared internal threonine-glutamic acid-threonine-proline repeat
 defines a family of Dictyostelium discoideum spore germination
 specific proteins";
 RL Biochemistry 29:7264-7269 (1990).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ax3;
 RA Giorda R., Ohmachi T., Shaw D.R., Ennis H.L.,
 RA Submitted (FEB-1995) to the EMBL/GenBank/DDJB databases.
 RL EMBL; U20661; ARB54078.1; -.
 DR dictyBase; DDB0187057; getE.
 DR InterPro; IPR00999; Actin_crosslink.
 KW Hypothetical protein.

SEQUENCE 460 AA; 51264 MW; 799492509ACCC66F6 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 460;
 Best Local Similarity 71.4%; Pred. No. 4.2e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PXRPXPL 8
 Db 72 PSRPyAL 78

RESULT 9

SYN_SUITO SYN_SUITO STANDARD; PRT; 540 AA.

ID SYN_SUITO STANDARD; PRT; 540 AA.

AC Q971D8; -.

DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--tRNA ligase beta chain) (PhERS).

GN Name=phe; OrderdLocusNames=STI415;

OS Sulfolobus tokodaii.

OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;

OC Sulfolobus.

OX NCBI_TaxID=11955;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=TCM 10545 / ?;

RX MEDLINE=21456156; PubMed=11574749;

RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Ankei A., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Onsuka R., Nakazawa H., Takamiya M., Fukui Y.,
 RA Yoshihwa T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT Complete genome sequence of an aerobic thermoacidophilic
 Crenarchaeon, Sulfolobus tokodaii strain7.;"

RL DNA Res. 8:123-140 (2001);
 CC -1- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA (Phe) = AMP +
 CC diphosphate + L-phenylalanyl-tRNA (Phe).
 CC -1- SUBUNIT: Trimer of two alpha and two beta chains (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cyttoplasmic.
 CC -1- SIMILARITY: Belongs to the phenylalanyl-tRNA synthetase beta chain
 CC family. Subfamily 2.

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EMBL; MF_00284; BAB66482.1; -.
 DR InterPro; IPR005147; B5.
 DR InterPro; IPR004531; PheT arch.
 DR InterPro; IPR00961; Putativ_DNA_bind.
 DR Pfam; PF03483; BS_4; 1.
 DR Pfam; PF03484; BS_1; 1.
 DR TIGRFAMS; TIGR00471; PheT arch; 1.
 KW Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;

Query Match	90.9%; Score 30; DB 1; Length 540;	Best Local Similarity 71.4%; Pred. No. 5e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	RN	NCBI_TaxID=44689;
Matches	5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	RN	SEQUENCE FROM N.A.	
Qy	2 PXRPyXL 8	RN	STRAIN=Ax3;	
Db	90 PSRPyYL 96	RN	Giorda R., Ohmachi T., Shaw D.R., Ennis H.L.; Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.	
RESULT 10		RL	DR	
ID 052305	PRELIMINARY; PRT; 569 AA.	DR	DR	
AC 052305;		DR	DR	
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)		DR	DictyBase; DDB0187057; gerB.	
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)		DR	GO; GO:005524; F-ATP binding; IEA.	
DE Urease alpha subunit.		DR	GO; GO:004672; :Protein kinase activity; IEA.	
GN Name=ureC;		DR	GO; GO:006468; Protein amino acid phosphorylation; IEA.	
OS Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).		DR	InterPro; IPR011009; Kinase_like.	
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.		KM	Hypothetical Protein.	
OX NCBI_TaxID=32049;		FT	NON TER 1 1	
RN [1]	SEQUENCE FROM N.A.	SQ	SEQUENCE 877 AA; 98709 MW; ECDB726FB1CA66CB CRC64;	
RP STRAIN=PCC 7002;		Query Match	90.9%; Score 30; DB 2; Length 877;	
RX MEDLINE=98320571; PubMed=9647800;		Best Local Similarity 71.4%; Pred. No. 8.6e-02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	RT	
RA Sakamoto T., Delaizco V.B., Bryant D.A.;		Qy	2 PXRPyXL 8	
RT Growth on urea can trigger death and peroxidation of the cyanobacterium Synechococcus sp. strain PCC 7002.";		Db	489 PSRPyYL 495	
RR -I- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3)		RESULT 12		
CC -I- COFACTOR: Binds 2 nickel ions per subunit (By similarity).		JAK3_RAT	STANDARD; PRT; 1100 AA.	
CC -I- SIMILARITY: Belongs to the urease family.		AC 06322;	DT 01-Nov-1997 (Rel. 35, Created)	
DR EMBL: AF035751; AAC26155.1; -.		DT 01-Nov-1997 (Rel. 35, Last sequence update)	DT 05-JUL-2004 (Rel. 44, Last annotation update)	
DR HSSP; PI8314; IEUK.		DE Tyrosine-Protein kinase JAK3 (EC 2.7.1.112) (Janus kinase 3) (JAK-3).	DE Tyrosine-Protein kinase JAK3 (EC 2.7.1.112) (Janus kinase 3) (JAK-3).	
DR GO; GO:0016787; F-hydrolase activity; IEA.		GN Name=JAK3;	GN Name=JAK3;	
DR GO; GO:0016511; F:nickel ion binding; IEA.		OS Rattus norvegicus (Rat).	OS Rattus norvegicus (Rat).	
DR GO; GO:0009039; F:urease activity; IEA.		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
DR GO; GO:0006807; P:nitrogen metabolism; IEA.		OC Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	OC Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
DR InterPro: IPR00680; Amidohydro_l.		OX NCBI_TaxID=10116;	OX NCBI_TaxID=10116;	
DR InterPro: IPR011059; Metallo_hydrolase.		RN [1]	RN [1]	
DR InterPro: IPR005849; Urease_alpha.		RP TISSUE=Spleen;	RP TISSUE=Spleen;	
DR InterPro: IPR008295; Urease_alpha_phalone.		RX MEDLINE=94192116; PubMed=8141963; DOI=10.1016/0014-5793(94)80485-0;	RX MEDLINE=94192116; PubMed=8141963; DOI=10.1016/0014-5793(94)80485-0;	
DR PIRSF; PIRSF011226; Urease_alpha; 1.		RA Takahashi T., Shirasawa T.;	RA Takahashi T., Shirasawa T.;	
DR PRINTS: PR01752; UREASE.		RT "Molecular cloning of rat JAK3, a novel member of the JAK family of RT "Molecular cloning of rat JAK3, a novel member of the JAK family of		
DR TIGRFAMs; TIGR01192; urease_alpha; 1.		RT FEBs Lett. 343:124-128 (1994).	RT FEBs Lett. 343:124-128 (1994).	
DR PROSITE; PS01120; UREASE_2; 1.		DT -I- FUNCTION: Tyrosine kinase of the non-receptor type, involved in the interleukin-2 and interleukin-4 signaling pathway.	DT -I- FUNCTION: Tyrosine kinase of the non-receptor type, involved in the interleukin-2 and interleukin-4 signaling pathway.	
DR PROSITE; PS01145; UREASE_2; 1.		CC Phosphorylates STAT6, IRS1, IRS2 and PI3K.	CC Phosphorylates STAT6, IRS1, IRS2 and PI3K.	
KW hydrolase; Metal-binding; Nickel.		CC -I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein	CC -I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein	
SQ SEQUENCE 569 AA; 61820 MW; DB717CA5B1642A93 CRC64;		CC tyrosin phosphat.	CC tyrosin phosphat.	
Query Match	90.9%; Score 30; DB 2; Length 569;	CC -I- SUBCELLULAR LOCATION: Wholly intracellular, possibly membrane associated (By similarity).	CC -I- SUBCELLULAR LOCATION: Wholly intracellular, possibly membrane associated (By similarity).	
Best Local Similarity 71.4%; Pred. No. 5.3e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		CC -I- TISSUE SPECIFICITY: Transcribed in a variety of tissues including spleen, lung, kidney and intestine.	CC -I- TISSUE SPECIFICITY: Transcribed in a variety of tissues including spleen, lung, kidney and intestine.	
Qy 2 PXRPyXL 8		CC -I- DOMAIN: Possesses two phosphotransferase domains. The second one probably contains the catalytic domain (By similarity), while the presence of slight differences suggest a different role for domain 1.	CC -I- DOMAIN: Possesses two phosphotransferase domains. The second one probably contains the catalytic domain (By similarity), while the presence of slight differences suggest a different role for domain 1.	
Db 302 PIPPyYL 308		CC -!- PTM: Tyrosine phosphorylated in response to IL-2 and IL-4 (By similarity).	CC -!- PTM: Tyrosine phosphorylated in response to IL-2 and IL-4 (By similarity).	
RESULT 11		CC -I- SIMILARITY: Belongs to the Tyr protein kinase family. JAK	CC -I- SIMILARITY: Contains 1 FERM domain.	
O23853 PRELIMINARY; PRT; 877 AA.		CC	CC	
ID 023853		CC	CC	
AC 023853;		CC	CC	
DT 01-NOV-1996 (TREMBLrel. 01, Created)		CC	CC	
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)		CC	CC	
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)		CC	CC	
OS Hypothetical protein (Fragment).		CC	CC	
OC Dictyostelium discoideum (Slime mold).		CC	CC	
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.		CC	CC	

-1- SIMILARITY: Contains 1 SH2 domain.

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CC EMBL; D28508; BA005868.1; -.

DR PIR; S43677; S43677.

DR HSSP; P11362; 1FGK.

DR RGD; 2940; Jak3.

DR InterPro; IPR000599; Band_4.1.

DR InterPro; IPR009127; JAK3.

DR InterPro; IPR009130; JAK3.

DR InterPro; IPR011009; Kinase like.

DR InterPro; IPR000719; prot_kinase.

DR InterPro; IPR000880; SH2.

DR InterPro; IPR001445; Tyr_pk kinase.

DR InterPro; IPR008266; Tyr_pk kinase_AS.

DR Pfam; PF0069; Pkinase_2.

DR PRINTS; PR01823; JANUSKINASE.

DR PRINTS; PR0102; JANUSKINASE3.

DR PRINTS; PR0109; TYRKINASE.

DR PRODOM; PD000001; Prt1.

DR PRODOM; PD000093; SH2; 1.

DR SMART; SMO295; B41; 1.

DR SMART; SMO295; SH2; 1.

DR SMART; SMO232; SH2; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 2.

DR PROSITE; PS5001; PROTEIN_KINASE_TYR; 1.

DR ATP-binding; Phosphorylation; Repeat; SH2 domain; Transferase; KW Tyrosine-protein kinase.

FT DOMAIN 24 353 FERM.

FT DOMAIN 372 472 SH2 (atypical).

FT DOMAIN 517 777 Protein kinase 1.

FT DOMAIN 818 1091 Protein kinase 2.

FT NIP BIND 824 832 ATP (By similarity).

FT BINDING 851 851 ATP (By similarity).

FT ACT SITE 945 945 Proton acceptor (By similarity).

FT MOD_RES 976 976 Phosphotyrosine (by autocatalysis) (By similarity).

FT SEQUENCE 1100 AA; 122560 MW; 1D59CA05F4DD7B2 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 1100; Best local Similarity 71.4%; Pred. No. 1.1e+03; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PXRPYXL 8 | ||| |

Db 228 PSRPYAL 234

RESULT 13

Q6MZA4 PRELIMINARY; PRT; 157 AA.

AC Q96MZA4; DT 01-DEC-2001 (TREMBIrel. 19', Created)

DT 01-DEC-2001 (TREMBIrel. 19', Last sequence update)

DT 25-OCT-2004 (TREMBIrel. 28, Last annotation update)

DE Hypothetical protein FLJ31659;

DE Name=FLJ31659;

OS Homo sapiens (Human);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.

NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX PMID=14702039; DOI=10.1038/ng1285;

RA Ota T., Suzuki Y., Nishikawa T., Ottuki T., Sugiyama T., Irie R., Yamamoto K., Yasuda T., Wayanggi T., Wagatsuma M., Makira K., Kimura K., Nagai K., Seine M., Obayashi M., Nishi T., Shiba T., Shirokane T., Tanaka T., Ishii S., Murakami K., Yauda T., Kodaira H., Kondo H., Sugawara M., Sudo H., Hosoi T., Kaku Y., Takeuchi K., Funuya T., Kikkawa E., Omura Y., Takahashi M., Kanda K., Yohoi T., Tanaka N., Saito K., Tanikawa M., Yamazaki M., Abe K., Kamihara K., Katsuta N., Saito K., Yamashita K., Murakawa K., Niromiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kinata M., Watanabe M., Hiraoaka S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Senoh T., Kubano S., Kuroda T., Ono Y., Takiguchi S., Watanabe M., Hiraoaka T., Yamashita K., Kamehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togita S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Musashino K., Yuki H., Oshima A., Sasaki S., Notsuka S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiono T., Sano S., Moriya S., Momiyama H., Satoch N., Terashima Y., Suzuki O., Nakagawa S., Senoh F., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Wakanae T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumada T., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Tashiro A., Taniguchi H., Tanigami A., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inada K., Ikeda Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Serba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Suano S.; RT "Complete sequencing and characterization of 21,243 full-length human cDNAs";

RL Nat. Genet. 36:40-45 (2004).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Prostate;

RX MEDLINE=23298257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold B.A., Grouse L.H., Dege J.G., Klausner R.D., Collins F.S., Wagner D., Schenner C.M., Schulz G.D., Altshuller S.P., Zeeberg B., Buetow K.H., Schaeffer C.F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loquelandano N.A., Peters G.J., Abramson R.D., Mullany S.J., Borak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Munro D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Scherich A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Prostate;

RA Strausberg R.; Submitted (FEB-2002) to the EMBL/Genbank/PDBJ databases.

DR EMBL; AK056221; BAB71123.1; -.

DR EMBL; BG02281; AAH2281.1; -.

KW Hypothetical Protein.

SQ SEQUENCE 157 AA; TDAGA84FP963BDF56 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 157; Best local Similarity 71.4%; Pred. No. 2e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PXRPYXL 8

Db 43 | ||| | PNRPYTL 49

RESULT 14
 Q03093 PRELIMINARY; PRT; 253 AA.
 AC Q03093;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Thioesterase.

OS Streptomyces hygroscopicus.
 OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1912;

RN [1] SEQUENCE FROM N.A.

RX MEDLINE:91294191; PubMed=2056341;
 RA Raibaud A., Zalacain M.M., Holt T.G., Tizard R., Thompson C.J.;
 RT "Nucleotide sequence analysis reveals linked N-acetyl hydrolase,
 thioesterase, transport, and regulatory genes encoded by the bialaphos
 RT biosynthetic gene cluster of Streptomyces hygroscopicus.";
 RL J. Bacteriol. 173:4454-4463(1991).

DR EMBL; MG4783; AAJ79278.1; -.
 DR PIR; C47031; C47031.

DR GO; GO:0016788; Fatty acid biosynthesis; IEA.

DR GO; GO:000958; P-biosynthesis; IEA.

DR SEQUENCE 253 AA; 27630 MW; 26602CDD0EFC2A3 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 253;
 Best Local Similarity 71.4%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
 Dd 78 PARPyVL 84

RESULT 15
 QTP853 PRELIMINARY; PRT; 257 AA.
 ID QTP853
 AC QTP853;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)

DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2).
 GN Name=FNT2185;
 OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
 OC NCBI_TaxID=209882;
 RN [1] SEQUENCE FROM N.A.

RC STRAIN=ATCC 49256;
 RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
 RA Haeckl R., Overbeek R., Kyriakis N.,
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

CC !-- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.

DR EMBL; AABF0100005; EA25081.1; -.

DR GO; GO:000317; CoA carboxylase complex; IEA.
 GO; GO:0003939; Facetyl-CoA carboxylase activity; IEA.

DR GO; GO:001674; F-ligase activity; IEA.
 GO; GO:0016740; F-ligase activity; IEA.

DR GO; GO:000663; P-fatty acid biosynthesis; IEA.

DR Interpro; IPR001995; Ag-CoA_carboxyA.

DR PRINTS; PP03255; ACCA; 1.

DR TIGRFAMS; TIGR00513; accA; 1.

DR Complete proteome; Ligase; Transferase.

SEQUENCE 312 AA; 34253 MW; 8DDE11C042DADA4 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 312;
 Best Local Similarity 71.4%; Pred. No. 4.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
 Dd 60 PDPRPyAL 66

RESULT 17
 Q8GCG99 PRELIMINARY; PRT; 313 AA.
 ID Q8GCG99
 AC Q8GCG99;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Acetyl-coenzyme A carboxyl transferase subunit alpha (EC 6.4.1.2).
 GN OrderidococcusName=FNT0409;
 OS Orderidococcus nucleatum (subsp. nucleatum).

OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;

DR PRINTS; PR01069; ACCCTFRASEA.

DR TIGRFAMS; TIGR00513; accA; 1.

OC Fusobacterium.
 OC NCB|_TAXID=76856;
 RN [1]
 RP SSEQUENCER FROM N.A.
 RC STRAIN=ATCC 25586;
 RX MEDLINE=21816394; PubMed=11889109;
 RT "genome sequence and analysis of the oral bacterium *Fusobacterium*
 RT nucleatum strain ATCC 25586.",
 RL J. Bacteriol. 184:2005-2018(2002).
 DR EMBL; AB010527; C:acetyl-CoA carboxylase complex; IEA.
 DR GO; GO:0009317; F:acetyl-CoA carboxylase activity; IEA.
 DR GO; GO:0003389; F:ligase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
 DR InterPro; IPR001095; Ac-CoA_carboxylA.
 DR Pfam; PF03255; ACCA; 1.
 DR PRINTS; PR01069; ACCCIRFRASEA.
 DR TIGRFAMS; TIGR00513; accA; 1.
 DR KW Complete proteome; Ligase; Transferase.
 SQ SEQUENCE 313 AA; 35303 MW; 878CFBC3F8DF261 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 313;
 Best Local Similarity 71.4%; Pred. No. 4.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXRPYXL 8
 Db 62 PERPYTL 68

RESULT 18

ID _ACCA_HABIN STANDARD; PRT; 315 AA.

AC P3872; DT 01-NOV-1995 (Rel. 32, Created)
 DT 25-OCT-2004 (Rel. 45, last annotation update)

DE Acetyl-coenzyme A carboxylase transferase subunit alpha
 (EC 6.4.1.2).
 Name=acca; OrderedLocusNames=H10406;
 OS *Haemophilus influenzae*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; *Haemophilus*.
 RN [1] - TAXID=727;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907; PubMed=7542800;
 RX MEDLINE=95350630; Adamo M.D., White O., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D., Scott J.D., Shizley R., Liu L.I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Heidelberg J., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Sudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M., Gnahm C.H., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
 RT "whole genome random sequencing and assembly of *Haemophilus influenzae* Rd.", Science 269:496-512 (1995).

-!- FUNCTION: This protein is a component of the acetyl coenzyme A carboxylase complex; first, biotin carboxylase catalyzes the carboxylation of the carrier protein and then the transcarboxylase transfers the carboxyl group to form malonyl-CoA (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate + malonyl-CoA.

RESULT 19

ID Q886M7 PRELIMINARY; PRT; 315 AA.

AC Q886M7; DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Acetyl-CoA carboxylase, carboxyl transferase, alpha subunit.
 GN Name=acca; OrderedLocusNames=PS010550;
 OS *Pseudomonas syringae* (pv. tomato).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
 OC NCB|_TAXID=323;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=DC3000;

RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100; Buell C.R., Joardar V., Lindberg M., Selengut J., Paulsen I.T., Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H., Nelson W.C., Davidsen T.M., Zafer N., Zhou L., Liu J., Yuan Q., Khouri H.M., Fedorova N.B., Tran B., Russell B., Berry K.J., Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Accenzo M., Deng W.J., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P., Laskarowitz S.G., Martin G.B., Schneider D.J.J., Tang X., Bender C.L., White O., Frazer C.M., Collier M.A., Schneider D.J.J., Tang X., RT "The complete genome sequence of the *Arabidopsis* and tomato pathogen *Pseudomonas syringae* pv. tomato DC3000.", Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
 RT EMBL; AR01681; AA055070.1; -. DR TIGR; PSPT01550; -. DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
 DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
 DR InterPro; IPR001095; Ac-CoA_carboxylA.

DR	PRINTS; PR01069; ACCCTRFASEA.
DR	TIGRFAMS; TIGR00513; accA; 1.
KW	Complete proteome; Transferase.
SQ	SEQUENCE 315 AA; 34975 MW; A878C54C71D5C555 CRC64;
QY	2 PXRPyXL 8
Db	67 PLRPYTL 73
RESULT 20	87.9%; Score 29; DB 2; Length 315; Best Local Similarity 71.4%; Pred. No. 4.5e+02; 2; Indels 0; Gaps 0;
Q8BMG4	PRELIMINARY; PRT; 315 AA.
ID	Q8BMG4; 01-JUN-2003 (TREMBrel. 24, Created)
AC	DT 01-JUN-2003 (TREMBrel. 24, Last sequence update)
DT	01-OCT-2003 (TREMBrel. 25, Last annotation update)
DB	Acetyl-CoA carboxylase, carboxyl transferase, alpha subunit.
GN	Name=accA; OrderedLocusNames=FP1607;
OS	Pseudomonas putida (strain KT2440).
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC	Pseudomonadaceae; Pseudomonas.
OX	NCBI_TaxID=160488;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=22422060; PubMed=12534463;
RA	Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F., Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M., Hance I., Chris Lee P., Holtzapfle E.K., Scenlan D., Tran K., Moestl D., Weidler H., Lauber J., Stjepanovic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B., Fraser C.M.;
RT	"Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440.";
RL	Environ. Microbiol. 4:79-80 (2002).
DR	EMBL; AS016779; AAN67228.1; -.
DR	TIGR; PP1607; -.
DR	GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
DR	GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR	GO; GO:005633; P:fatty acid biosynthesis; IEA.
DR	InterPro; IPR010982; Lambda_Like_DNA.
DR	InterPro; IPR010982; Lambda_Like_DNA.
DR	InterPro; IPR010982; Lambda_Like_DNA.
DR	PRINTS; PR01069; ACCCTRFASEA.
DR	PRINTS; PR01069; accA; 1.
DR	TIGRFAMS; TIGR00513; accA; 1.
DR	Complete proteome.
SQ	SEQUENCE 315 AA; 35135 MW; 65952AE13959BDAD CRC64;
Query Match	87.9%; Score 29; DB 2; Length 315; Best Local Similarity 71.4%; Pred. No. 4.5e+02; 2; Indels 0; Gaps 0;
Matches	5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	2 PXRPyXL 8
Db	67 PLRPYTL 73
RESULT 22	87.9%; Score 29; DB 2; Length 315; Best Local Similarity 71.4%; Pred. No. 4.5e+02; 2; Indels 0; Gaps 0;
Q9HKZ2	PRELIMINARY; PRT; 316 AA.
ID	Q9HKZ2; 01-MAR-2001 (TREMBrel. 16, Created)
AC	DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)
DT	01-JUN-2003 (TREMBrel. 24, Last annotation update)
DE	Acetyl-coenzyme A carboxylase carboxyl transferase (Alpha subunit).
GN	Name=accA; OrderedLocusNames=PA0639;
OS	Pseudomonas aeruginosa.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC	Pseudomonadaceae; Pseudomonas.
OX	NCBI_TaxID=287;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RC	STRAIN=ATCC 15692 / PAO1;
RC	STOVER C.K., PHAM X.-Q.T., ERWIN A.L., MICOGUCHI S.D., WARRENER P., HICKEY M.J., BRINKMAN F.S.L., HUFNAGLE W.O., KOWALIK D.J., LAGROU M., GARBER R.L., GOLTRY L., TOLENTINO E., WESTBROOK-WADMAN S., YUAN Y., BRODY L.L., COULTER S.N., FOLGER K.R., KAS A., LARBIG K., LIM R.M., SMITH K.A., SPENCER D.H., WONG G.K.-S., WU Z., PAULSEN I.T., REIZNER J., SAUER M.H., HANCOCK R.E.W., LORY S., OLSON M.V.;
RT	"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
RT	Nature 406:939-964 (2000).
DR	EMBL; AS004783; AAG07027.1; -.
DR	PIR; DB3192; DB3192.
DR	GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
DR	GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR	GO; GO:0016740; P:fatty acid biosynthesis; IEA.
DR	GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR	InterPro; IPR001095; AC-CoA_carboxyla.

DR Pfam; PF0325; ACCA; 1.
 DR PRINTS; PR01069; ACCCPRFSEA.
 DR TIGRFAMS; TIGR00513; acca; 1.
 KW Complete proteome; Transferase.
 SQ SEQUENCE 316 AA; 34947 MW; 914D9418A79FB484 CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 316;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 67 PKRPyTL 73

RESULT 23

QTVPL3 PRELIMINARY; PRT; 317 AA.

ID QTVPL3
 AC QTVPL3;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DE Acetyl-CoA carboxylase carboxyl transferase subunit alpha.
 GN Name=acca; OrderedLocusNames=HD0051;
 OS Haemophilus ducreyi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=730;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN35000SP / ATCC 700724;
 RA Munson, R.S., Ray, W.C., Mahairas, G., Sabo, P., Mungur, R.,
 RA Johnson, L., Nguyen, D., Wang, J., Forst, C., Hood, L.;
 RT "The complete genome sequence of *Haemophilus ducreyi*";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017151; AAP95066.1; -.
 DR GO; GO:0009317; Clacetyl-CoA carboxylase complex; IEA.
 DR GO; GO:0009389; Fatty acid biosynthesis; IEA.
 DR GO; GO:0015740; Fatty acid transferase activity; IEA.
 DR GO; GO:0006633; Fatty acid biosynthesis; IEA.
 DR InterPro; IPR01095; Ac-CoA carboxyla.
 DR InterPro; IPR01092; Lambda-like DNA.
 DR Pfam; PF03255; ACCA; 1.
 DR TIGRFAMS; TIGR00513; acca; 1.
 KW Complete proteome; Transferase.
 SQ SEQUENCE 317 AA; 35212 MW; 3DFB30A7680879C6 CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 317;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 24

QP2H6 PRELIMINARY; PRT; 317 AA.

ID QP2H6
 AC QP2H6;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE ACCA protein.
 GN Name=acca; OrderedLocusNames=WIGBR3780;
 OS Wiggleworthia glossinidria brevipalpis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Wiggleworthia.
 OX NCBI_TaxID=36870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-2297718; PubMed=12219091; DOI=10.1038/ng986;
 RA Akhman, L., Yamashita, A., Watanabe, H., Ohshima, K., Shiba, T., Hattori, M.,

RA Akhoy, S.;
 RT "Genome sequence of the endocellular obligate symbiont of tsetse files, *Wigglesworthia glossinidria*";
 RT Nat. Genet. 32:442-447(2002);
 RL Nat. Genet. 32:442-447(2002);
 DR EMBL; AB063522; BRCA2424.1; -.
 DR GO; GO:0009317; Clacetyl-CoA carboxylase complex; IEA.
 DR GO; GO:0003889; Fatty acid biosynthesis; IEA.
 DR GO; GO:0006633; Fatty acid biosynthesis; IEA.
 DR InterPro; IPR010195; Ac-CoA carboxyla.
 DR InterPro; IPR010882; Lambda-like DNA.
 DR Pfam; PF03255; ACCA; 1.
 DR PRINTS; PR01069; ACCCPRFSEA.
 DR TIGRFAMS; TIGR00513; acca; 1.
 KW Complete proteome.
 SQ SEQUENCE 317 AA; 35637 MW; 26588C43A815091B CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 317;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 68 PMRPyTL 74

RESULT 25

Q9CNX9 PRELIMINARY; PRT; 317 AA.

ID Q9CNX9
 AC Q9CNX9;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DR Acca.
 GN Name=acca; OrderedLocusNames=PM0292;
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-Pm70;
 RA MEDLINE-2115866; PubMed=11248100; DOI=10.1073/pnas.051634598;
 RA May, B.J., Zhang, Q., Li, L.I., Paustian, M.L., Whittem, T.S., Kapoor, V.,
 RT "Complete genomic sequence of *Pasteurella multocida* Pm70";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 DR EMBL; AB06064; AAK02376.1; -.
 DR GO; GO:0009317; Clacetyl-CoA carboxylase complex; IEA.
 DR GO; GO:0003889; Fatty acid biosynthesis; IEA.
 DR GO; GO:0006633; Fatty acid biosynthesis; IEA.
 DR InterPro; IPR001035; Ac-CoA carboxyla.
 DR InterPro; IPR000577; FGGY kin.
 DR InterPro; IPR01092; Lambda-like DNA.
 DR Pfam; PF03255; ACCA; 1.
 DR PRINTS; PR01069; ACCCPRFSEA.
 DR TIGRFAMS; TIGR00513; acca; 1.
 KW Complete proteome; FGGY_KINASES_2; UNKNOWN_1.
 SQ SEQUENCE 317 AA; 35341 MW; F8B3DDA93723D1F6 CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 317;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 68 PNRPyTL 74

RESULT 26

ACCA_ECOLI PRELIMINARY; PRT; 318 AA.

ID ACCA_ECOLI
 ID ACCA_ECOLI STANDARD;
 AC P30867;
 DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, last sequence update)
 DT 25-JAN-2005 (Rel. 46, last annotation update)

DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
 DE (EC 6.4.1.2).

DN Name=accB; OrderedLocusName=b0185, z0197, ECs0187, SF0175, S0178;

OS Escherichia coli,
 OS *Escherichia coli* O157:H7, and
 OS *Shigella flexneri*.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OK NCBI_TaxID=562, 83334, 623;

RN [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC SPECIES=E.coli; STRAIN=K12 / W3110;

RX MEDLINE=92380982; PubMed=1355089;

RA Li, S.-J.; Cronan, J. E. Jr.;

RT "The genes encoding the two carboxyltransferase subunits of
Escherichia coli acetyl-CoA carboxylase.";

RL *J. Biol. Chem.* 267:16841-16847(1992).

RN [2] SEQUENCE FROM N.A.

RP SPECIES=E.coli; STRAIN=K12 / W3110;

RC SPECIES=E.coli; STRAIN=K12 / W3110;

RA Yamamoto, Y.; Submitted (DPC-1995) to the EMBL/GenBank/DBJ databases.
 [3]

RN SEQUENCE FROM N.A.

RC SPECIES=E.coli; STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;

RA Blattner, F.R.; Plunkett, G. III; Bloch, C.A.; Perna, N.T.; Burland, V.;
 RA Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.;

RA Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Geeden, M.A.; Rose, D.J.;

RA Mai, B.; Shao, Y.;

RA "The complete genome sequence of *Escherichia coli* K-12.";

RL *Science* 277:1453-1474(1997).

RN [4]

RP SEQUENCE FROM N.A.

RC SPECIES=E.coli; STRAIN=K12 / W3110;

RA Takeimoto, K.; Mori, H.; Murayama, N.; Kataoka, K.; Yano, M.; Itoh, T.;
 RA Yamamoto, Y.; Inokuchi, H.; Maki, T.; Hatada, E.; Fukuda, R.; Ichihara, S.,
 RA Mizuno, T.; Makino, K.; Nakata, A.; Yura, T.; Sampei, G.; Mizobuchi, K.;

RT "Systematic sequencing of the *Escherichia coli* genome: analysis of the
 RT 4.0 - 6.0 min (189,987 - 281,416pp) region.";

RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 [5]

RN SEQUENCE FROM N.A.

RC SPECIES=E.coli;

RA Schramm, S.; Duncan, M.; Allen, B.; Araujo, R.; Aparicio, A.; Chung, E.;
 RA Lashkari, D.; Lew, H.; Lin, D.; Namath, A.; Oetther, P.; Roberts, D.;
 RA Davis, R.W. (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RL [6]

RP SEQUENCE FROM N.A.

RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;

RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/z3505089;

RA Perna, N.T.; Plunkett, G. III; Burland, V.; Mai, B.; Glasner, J.D.;

RA Rose, D.J.; Mayhew, G.F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.;

RA Pfeifer, G.; Hackett, J.; Klink, S.; Boutin, A.; Shao, Y.; Miller, L.;

RA Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimaranta, E.T.; Potamitis, K.;

RA Apodaca, J.; Anantharaman, T.S.; Lin, J.; Yen, G.; Schwartz, D.C.;

RA Welch, R.A.; Blattner, F.R.;

RT "Genome Sequence of enterohemorrhagic *Escherichia coli* O157:H7.";

RL *Nature* 409:p529-533(2001).

RN [7] SEQUENCE FROM N.A.

RC SPECIES=E.coli; STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;

RX MEDLINE=21156231; PubMed=11258796;

RA Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.,
 RA Iida, T.; Takami, H.; Honda, T.; Sabikawa, C.; Ogasawara, N.; Yasunaga, T.,
 RA Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.; Shinagawa, H.;
 RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*
 RT 0157:H7 and genomic comparison with a laboratory strain K-12.";

RL DNA Res. 8:11-22(2001).
 RN [8] SEQUENCE OF 163-318 FROM N.A.

RC SPECIES=E.coli; STRAIN=K12 / W3110;

RX MEDLINE=9736816; PubMed=9226257;

RA Kikuchi, Y.; Kojima, H.; Tanaka, T.; Takatsuka, Y.; Kamio, Y.;

RT "Characterization of a second lysine decarboxylase isolated from
Escherichia coli.";

RL *J. Bacteriol.* 179:4486-4492(1997).

RN [9] SEQUENCE OF 1-12; STRAIN=K12 / EMG2;

RC SPECIES=E.coli; STRAIN=K12 / W3110;

RX MEDLINE=97443975; PubMed=9298646;

RA Link, A.J.; Robison, K.; Church, G.M.;

RT "Comparing the predicted and observed properties of proteins encoded
 in the genome of *Escherichia coli* K-12.";

RL *Electrophoresis* 18:1259-1313(1997).

RN [10] SEQUENCE FROM N.A.

RC SPECIES=S.Flexneri; STRAIN=301 / Serotype 2a;

RX MEDLINE=22272406; PubMed=12384530; DOI=10.1093/nar/gkf565;

RA Jin, Q.; Yuan, Z.; Xu, J.; Wang, Y.; Shen, Y.; Lu, W.; Wang, J.; Liu, H.;

RA Yang, J.; Yang, F.; Zhang, X.; Zhang, J.; Yang, G.; Wu, H.; Qu, D.; Dong, J.;

RA Sun, L.; Xue, Y.; Zhao, A.; Gao, Y.; Zhu, J.; Kan, B.; Ding, K.; Chen, S.;

RA Cheng, H.; Yao, Z.; He, B.; Chen, R.; Ma, D.; Qiang, B.; Wen, Y.; Hou, Y.;

RA Yu, J.;

RT "Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity
 through comparison with genomes of *Escherichia coli* K12 and O157.";

RL Nucleic Acids Res. 30:4432-4441(2002).

RN [11] SEQUENCE FROM N.A.

RC SPECIES=S.Flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;

RX MEDLINE=22590274; PubMed=12704152;

DOI=10.1128/JAI.71.5.2775-2786.2003;

RA Wei, J.; Goldberg, M.B.; Burland, V.; Venkatesan, M.M.; Deng, W.;
 RA Fournier, G.; Mayhew, G.F.; Plunkett, G. III; Rose, D.J.; Darling, A.;

RA Mau, B.; Perna, N.T.; Payne, S.M.; Runyen-Janecky, L.J.; Zhou, S.;
 RA Schwartz, D.C.; Blattner, F.R.;

RT "Complete genome sequence and comparative genomics of *Shigella*
flexneri serotype 2a strain 2457T.";

RL *Infect. Immun.* 71:2775-2786(2003).

CC --!- FUNCTION: This protein is a component of the acetyl coenzyme A
 CC carboxylase complex; first, biotin carboxylase catalyzes the
 CC carboxylation of the carrier protein and then the transcarboxylase
 CC transfers the carboxyl group to form malonyl-CoA.

CC --!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) (-) = APP + phosphate
 CC + malonyl-CoA.

CC --!- SUBUNIT: Long-chain fatty acid biosynthesis; first step.

CC --!- CARBON-CARRIER: Acetyl-CoA carboxylase is an heterohexameric of biotin
 CC carboxyl carrier protein, biotin carboxylase and the two subunits
 CC of carboxyl transferase in a 2:2 complex.

CC --!- SIMILARITY: Belongs to the accA family.

CC --!- SIMILARITY: Contains 1 acetyl-coenzyme A carboxyltransferase Cter
 domain.

CC -----

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DR EMBL: M06394; AAC070370; 1; -;

DR EMBL: D03536; BA07860; 1; -;

DR EMBL: U0096; AAC0296; 1; -;

DR EMBL: U0214; AA080614; 1; -;

DR EMBL: AB005194; AAQ5487; 1; -;

DR EMBL: AB002550; BAB33610; 1; -;

DR EMBL: D07518; BA21655; 1; -;

DR EMBL: AB015054; AAC41337; 1; -;

DR EMBL: AB016978; AAP15718; 1; -;

DR PIR; A43452; A43452.
 DR C85503; C85503.
 DR PIR; C90652; C90652.
 DR EchoBASE; EB1600; -.
 DR Ecogene; EG11647; acca.
 DR InterPro; IPR001095; Ac-CoA _ carboxylyA.
 DR PR03255; ACCA; 1.
 DR PRINTS; PR01069; ACCCIRFRASEA.
 DR TIGRFAMS; TIGR00513; acca; 1.
 DR PROSITE; PSS0989; COA CT CTER; 1.
 KW Complete proteome; Direct protein sequencing; Fatty acid biosynthesis; Ligase.
 FT INIT_MER 0 0
 FT DOMAIN 83 118 Acyl-CoA-binding domain (Potential).
 FT DOMAIN 24 24 V->G (in Ref. 4).
 FT CONFLICT 318 AA; 35110 MW; 8938B808E5B3C9AD CRC64;
 SQ Sequence 318 AA; 35110 MW; 8938B808E5B3C9AD CRC64;

Query Match
 Best local similarity 87.9%; Score 29; DB 1; Length 318;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 CC
 Qy 2 PXRXPXL 8
 Db 69 PORPYTL 75

RESULT 27
 ACCA_SALTY STANDARD PRT; 318 AA.
 ID ACCA_SALTY PRT; 318 AA.
 AC PA0674;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
 DE (EC 6.4.1.12).
 GN Name=acca; OrderedLocusNames=STM0232, STY0255, t0233;
 OS *Salmonella* typhimurium, and
 OS *Salmonella* Typhi.
 OC Bacterium; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Salmonella*.
 OX NCBI_TaxID=602, 601;
 RN [1]
 RP Sequence from N.A.
 RC SPECIES=S.TYPHIMURIUM; STRAIN=LIT2 / SGSC142 / ATCC 700720;
 RX MEDLINE:21534948; PubMed=1677609; DOI=10.1038/35101614;
 RA McClelland M.; Sanderston K.E.; Spieth J.; Clifton S.W.; Latreille P.;
 RA Courtney L.; Porwollik S.; Ali J.; Dante M.; Du F.; Hou S.; Layman D.;
 RA Leonard S.; Nguyen C.; Scott K.; Holmes A.; Grewal N.; Milvane E.;
 RA Ryan E.; Sun H.; Florea L.; Miller W.; Stonking T.; Nhan M.;
 RA Waterston R.; Wilson R.K.; Miller W.; Stonking T.; Nhan M.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 RT LIT2.";
 RL Nature 413:852-856(2001).
 RN [2]
 RP Sequence of 1-35 from N.A.
 RC SPECIES=S.TYPHIMURIUM;
 RX MEDLINE:90008797; PubMed=2676978;
 RA Lancy E.D.; Lifschis M.R.; Munson P.; Maurer R.;
 RT "Nucleotide sequence of dnaE, the gene for the polymerase subunit of DNA polymerase III in *Salmonella typhimurium*, and a variant that facilitates growth in the absence of another polymerase subunit.";
 RT J. Bacteriol. 171:5581-5586(1989).
 RL
 RN [3]
 RP Sequence from N.A.
 RC SPECIES=S.TYPHI; STRAIN=CT18;
 RX MEDLINE:21534947; PubMed=11677608; DOI=10.1038/35101607;
 RA Parkhill J.; Dougan G.; James K.B.; Thomson R.; Pickard D.; Wain J.;
 RA Churcher C.M.; Mungall K.L.; Bentley D.S.; Holden M.T.G.; Sebaihia M.;
 RA Baker S.; Basham D.; Brooks D.; Chillingworth T.; Connerton P.;
 RA Cronin A.; Davis P.; Davies R.M.; Dowd L.; White N.; Farrar J.;
 RA Feltwell T.; Hamlin N.; Hague A.; Hien T.T.; Holroyd S.; Jagels K.;
 RA Krogh A.; Larsen T.S.; Leather S.; Moile S.; O'Gaoora P.; Parry C.;
 RA Quail M.A.; Rutherford K.M.; Simmonds M.; Skelton J.; Stevens K.,
 RA Whitehead S.; Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella* enterica serovar Typhi CT18.";
 RT Nature 413:848-852(2001).

[4]

RN Sequence from N.A.
 RC SPECIES=S.TYPHI; STRAIN=TY2 / ATCC 700931;
 RC MEDLINE=22331367; PubMed=1264504;
 RX DOI=10.1128/JB.185.7.2330-2337.2003;
 RA Deng W.; Liou S.-R.; Plunkett G. III; Mayhew G.F.; Rose D.J.;
 RA Burland V.; Kodoyani V.; Schwartz D.C.; Blattner F.R.;
 RT "Comparative genomics of *Salmonella enterica* enterica serovar Typhi strains TY2 and TY8.";
 RL J. Bacteriol. 185:2330-2337(2003).

CC -!- FUNCTION: This protein is a component of the acetyl coenzyme A carboxylase complex; first, biotin carboxylase catalyzes the carboxylation of the carrier protein and then the transcarboxylase transfers the carboxyl group to form malonyl-CoA.

CC -!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate + malonyl-CoA.

CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.

CC -!- SUBUNIT: Acetyl-CoA carboxylase is an heterohexamer of biotin carboxyl carrier protein, biotin carboxylase and the two subunits of carboxyl transferase in a 2:2 complex.

CC -!- SIMILARITY: Belongs to the acca family.

CC -!- SIMILARITY: Contains 1 acetyl-coenzyme A carboxyltransferase Cter domain.

CC -----

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CC -----

DR EMBL; AB008705; RAL19196.1; -.
 DR EMBL; M26046; -, NOT_ANNOTATED_CDS.
 DR EMBL; AU627266; CRD00890.1; -.
 DR EMBL; AB16834; RAO67963.1; -.
 DR StyGene; SG10496; acca.
 DR InterPro; IPR00195; Ac-CoA_carboxylyA.
 DR PR03255; ACCA; 1.
 DR PRINTS; PR01069; ACCCIRFRASEA.
 DR TIGRFAMS; TIGR00513; acca; 1.
 DR PROSITE; PSS0989; COA CT CTER; 1.
 KW Complete proteome; Fatty-acid biosynthesis; Ligase.
 FT INIT_MER 0 0 By Similarity:
 FT DOMAIN 83 118 Acyl-CoA-binding domain (Potential).
 FT DOMAIN 16 16 A->R (in Ref. 2).
 FT CONFLICT 16 16 A->R (in Ref. 2).
 SQ Sequence 318 AA; 3512 MW; 749B990EC01F9D0 CRC64;

Query Match
 Best local similarity 87.9%; Score 29; DB 1; Length 318;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 CC
 Qy 2 PXRXPXL 8
 Db 69 PORPYTL 75

RESULT 28
 Q667K5 PRELIMINARY PRT; 319 AA.
 ID Q667K5
 AC 0667K5;
 DT 25-OCT-2004 (TREMBrel. 28, Created)
 DT 25-OCT-2004 (TREMBrel. 28, Last sequence update)
 DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit al. . . (EC 6.4.1.2).
 GN Name=acca; ORFNames=YPRB2977;
 OG *Versinia pseudotuberculosis* IP 32953
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=273123;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TP 3253;
 RK PUBMED=15358958;
 RA Chain P.S.G., Carmel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
 RA Regal M.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
 RA Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., Medigue C.,
 RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
 RA Derbise A., Hauser J.J., Garcia E.,
 RT "Insights into the genome evolution of *Yersinia pestis* through whole
 genome comparison with *Yersinia pseudotuberculosis*";
 PRO. Natl. Acad. Sci. U.S.A. 101:13826-13831 (2004).
 RL DR
 DR GO: GO:0016874; Fl-ligase activity; IEA.
 DR GO: GO:0016874; Fl-transferase activity; IEA.
 DR InterPro; IPR01035; Ac-CoA carboxyla.
 DR Pfam; PF03255; ACCA; 1.
 DR PRINTS; PR1069; ACCCTFRASEA.
 DR TIGRFAMS; TIGR00513; acca; 1.
 KW Ligase; Transferase.
 SQ SEQUENCE 319 AA; 35495 MW; 45ABB190ECB7B402E CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXRPyXL 8
 QD |||||
 DR 70 PRRPyTL 76
 RESULT 29
 Q8PAW9 PRELIMINARY; PRT; 319 AA.
 ID Q8PAW9
 AC Q8PAW9;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DB Acetyl-coenzyme A carboxylase carboxyl transferase.
 GN Name=ACCA; OrderedLocusNames=XACI3405;
 OS Xanthomonas axonopodis (pv. citri).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=92829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=306 / ATCC 13902 / XV 101;
 RX MEDLINE=2002145; PubMed=12024217; DOI=10.1038/417459a;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.B., do Amaral M.E., Bartolini M.C., Camargo L.E.A.,
 RA Camarotte G., Canavan F., Cardozo J., Chambergo F., Cipolla L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Curitino-Santos J.R., El-Dorry H.,
 RA Faria J.B., Ferreria A.J.S., Ferreira R.C.C., Ferro M. I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katayama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Medanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Souza R.F.,
 RA Spinola L.A.P., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.,
 RT "Comparison of the genomes of two *Xanthomonas* pathogens with differing
 host specificities";
 RT Nature 417:459-463 (2002).
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katayama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Medanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Souza R.F.,
 RA Spinola L.A.P., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.,
 RT "Comparison of the genomes of two *Xanthomonas* pathogens with differing
 host specificities";
 RL Nature 417:459-463 (2002).
 DR EMBL; AB012234; AdM406551; -.
 DR GO: GO:0009317; C-acetyl-CoA carboxylase complex; IEA.
 DR GO: GO:0003989; Fatty-acyl-CoA carboxylase activity; IEA.
 DR GO: GO:0006633; P-fatty acid biosynthesis; IEA.
 DR InterPro; IPR001095; Ac-CoA carboxyla.
 DR Pfam; PF03255; ACCA; 1.
 DR PRINTS; PR1069; ACCCTFRASEA.
 DR TIGRFAMS; TIGR00513; acca; 1.
 KW Complete proteome.
 SQ SEQUENCE 319 AA; 35270 MW; 385DBBBABEA0DC3 CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Q8ZH52 PRELIMINARY; PRT; 319 AA.
 ID Q8ZH52; Q7CH51; Q7CH19;
 AC Q7CH51;
 DT 01-MAR-2002 (TREMBrel. 20, Created)
 DT 01-MAR-2002 (TREMBrel. 20, Last sequence update)
 DT 25-OCT-2004 (TREMBrel. 28, Last annotation update)
 DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2) (Acetyl CoA carboxylase, carboxytransferase component, alpha subunit)
 DE subunit); OrderedLocusNames=YP2790, YP0160, Y3119;
 GN Name=acCA; OrderedLocusNames=YP2790, YP0160, Y3119;
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.
 OC Enterobacteriaceae; Yersinia.
 OC NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis; PubMed=11586360; DOI=10.1038/35097083;
 RX MEDLINE=21470413;
 RA Parkhill J., Wren B.W., Thomson N.R., Titchall R.W., Holden M.T.G., Prentice M.B., Sebaihi M., James K.D., Churcher C.M., Mungall K.L., Baker S., Basham D., Bentley D., Brooks J., Cerdeno-Tarraga A.-M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Immonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; RA RT Genome Sequence of Yersinia pestis, the causative agent of plague. ";
 RL Nature 413:523-527(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIM5 / Biovar Mediaevalis; MEDLINE=2217863; Pubmed=12142430;
 RX DOI=10.1128/JB.148.16_4601-4611.2002;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fletcherston J.D., Lindner L.B., Brubaker R.R., Piano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R., RA Perry R.D.; RT Genome sequence of Yersinia pestis KIM.";
 RL J. Bacteriol. 184:4601-4611(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=91001 / Biovar Mediaevalis; Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D., RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z., RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P., RA Yang R.; RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AU41446; CACB89902.1; -. DR EMBL; AE013912; AAM86659.1; -. DR EMBL; AE017137; AAS62974.1; -. DR PTB; AC0130; AC0130.
 DR GO; GO:0009317; Cl-acetyl-CoA carboxylase complex; IEA. DR GO; GO:003989; Fattyacyl-CoA carboxylase activity; IEA. DR GO; GO:0016874; Filigase activity; IEA. DR GO; GO:0016740; F-transferase activity; IEA. DR GO; GO:0006633; F-fatty acid biosynthesis; IEA. DR PRINTS; PRO1069; ACCCFRASEA. DR TIGRFAM; TIGR00513; acCA; 1. DR Complete proteome; Disease; Transferase. SQ SEQUENCE 319 AA; 35595 MW; 45ABBL90ETCB402E CRC64;

Query Match Score 87.9%; Best Local Similarity 87.9%; Score 29; DB 2; Length 319; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 2 PXRDXL 8 Db 70 PRRPYTL 76

RESULT 33
 Q7N8N1 PRELIMINARY; PRT; 319 AA.
 ID Q7N8N1;
 AC Q7N8N1;
 DT 01-MAR-2004 (TREMBrel. 26, Created)
 DT 01-MAR-2004 (TREMBrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 DE Acetyl-CoA carboxylase alpha subunit; Name=acCA; OrderedLocusNames=plu0688; OS Photorhabdus luminescens (subsp. laumondii). OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus. OC NCBI_TaxID=141679;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TTO1; MEDLINE=2295627; PubMed=14528314;
 RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A., TAOURIT S., BOCS S., BOURBAU-EDE C., CHANDLER M., CHARLES J.-F., DAUSA E., DEROUZE R., DERZELLE S., FROYSSINET G., GAUDRAULT S., RA MEDIGUE C., LANOIS A., POWELL K., SQUIER P., VINCENT R., WINGATE V., ZOUINE M., GLASER P., BOEMARE N., DANCHIN A., KUNST F.; RT "The genome sequence of the entomopathogenic bacterium Photorhabdus luminescens"; Nat. Biotechnol. 21:1207-1213 (2003).
 RL BACTECHNOL. 21:1207-1213 (2003).
 DR EMBL; BX571861; CABE12983.1; -. DR Photolist; BL00688; -. DR GO; GO:0009317; Cl-acetyl-CoA carboxylase complex; IEA. DR GO; GO:003989; Fattyacyl-CoA carboxylase activity; IEA. DR GO; GO:0006633; F-fatty acid biosynthesis; IEA. DR InterPro; IPR001095; AC-CoA_carboxyla. DR Pfam; PF03255; acCA; 1. DR PRINTS; PRO1069; ACCCFRASEA.

Query Match Score 87.9%; Best Local Similarity 71.4%; Pred No. 4.5e+02; Length 319; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0; QY 2 PXRDXL 8 Db 70 PRRPYTL 76

RESULT 32
 Q7MH6 PRELIMINARY; PRT; 319 AA.
 ID Q7MH6;
 AC Q7MH6;
 DT 01-MAR-2004 (TREMBrel. 26, Created)
 DT 01-MAR-2004 (TREMBrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 DE Acetyl-CoA carboxylase alpha subunit; Name=acCA; OrderedLocusNames=VV2540; OS Vibrio vulnificus (strain YJ016). OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; OC Vibrionaceae; Vibrio. OC NCBI_TaxID=196600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=1465965; DOI=10.1101/gr.1295503;
 RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C., Su T.-L., Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.-B.-T., Li J.-C., Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-P.; RT Comparative genome analysis of Vibrio vulnificus, a marine pathogen. ";; RQ Genome Res. 13:2577-2587 (2003).
 DR EMBL; AU005340; BAC9504.1; -. DR GO; GO:0009317; Cl-acetyl-CoA carboxylase complex; IEA. DR GO; GO:003989; Fattyacyl-CoA carboxylase activity; IEA. DR GO; GO:006333; Fattyacyl-CoA biosynthesis; IEA. DR INTERPRO; IPR001095; Ac-CoA_carboxyla. DR PFAM; PF03255; acCA; 1. DR PRINTS; PRO1069; ACCCFRASEA. DR TIGRFAM; TIGR00513; acCA; 1. DR Complete proteome; SEQENCE 319 AA; 35572 MW; 25D56FDDB230DC138 CRC64;

Query Match Score 87.9%; Best Local Similarity 71.4%; Pred No. 4.5e+02; Length 319; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0; QY 2 PXRDXL 8 Db 70 PRRPYTL 76

DR TIGRFAMS; TIGR00513; accA; 1.
 KW Complete proteome.
 SQ SEQUENCE 319 AA; 35523 MW; EIF08BF0F45FCE2 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PXRPYXL 8
 Db 70 PRRPYTL 76

RESULT 34
 OYVRD0 PRELIMINARY; PRT; 319 AA.

ID OYVRD0; PRELIMINARY; PRT; 319 AA.

AC OYVRD0; PRELIMINARY; PRT; 319 AA.

DT 01-OCT-2003 (TREMBrel. 25, Created)
 DT 01-OCT-2003 (TREMBrel. 25, Last sequence update)

DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2).
 DE Name=accA; OrderedlocusNames=Bfl1287;
 GS Candidatus Blochmannia florianus

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobactiales;
 OC Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
 RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-22784745; PubMed=12886019; DOI=10.1073/pnas.1533499100;
 RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,
 RA Latorre A., Rausell C., Kammerbeek J., Gadau J., Hoelldobler B.,
 RA van Ham R.C.H.J., Gross R., Moya A.;
 RT "The genome sequence of *Blochmannia florianus*: comparative analysis
 of reduced genomes";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:9389-9393 (2003).

DR EMBL; BX248585; CAD83358.1; -.

DR GO; GO:0009317; Cacyetyl-CoA carboxylase complex; IEA.

DR GO; GO:0003989; F-acetyl-CoA carboxylase activity; IEA.

DR InterPro; IPR01035; Ac-CoA_carboxyla.

DR Pfam; PF03255; ACCA; 1.

DR TIGRFAMS; TIGR00513; accA; 1.

KW Complete proteome.

SQ SEQUENCE 319 AA; 35813 MW; 1DB9B1C7CCEA3A9C CRC64;

Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PXRPYXL 8
 Db 70 PRRPYTL 76

RESULT 35
 O87MF3 PRELIMINARY; PRT; 319 AA.

ID O87MF3; PRELIMINARY; PRT; 319 AA.

AC O87MF3; PRELIMINARY; PRT; 319 AA.

DT 01-JUN-2003 (TREMBrel. 24, Created)
 DT 01-JUN-2003 (TREMBrel. 24, Last sequence update)

DE Acetyl-CoA carboxylase, carboxyl transferase alpha subunit.
 GS OrderedlocusNames=VP2302;

OC Bacteroides parahemolyticus

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.

RN NCBI_TaxID=670;
 RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=RIMD 2210633 / Serotype 03:K6;
 RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
 RA Makino K., Ohshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Iijima Y., Nagima M., Nomura M., Yamashita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,
 RT "Genome sequence of *Vibrio parahaemolyticus*: a pathogenic mechanism
 RT distinct from that of *V. cholerae*";
 RL Lancet 361:743-749 (2003).

DR EMBL; AP005081; BAC6065.1; -.

DR GO; GO:0009317; Cacyetyl-CoA carboxylase complex; IEA.

DR GO; GO:0003989; F-acetyl-CoA carboxylase activity; IEA.

DR GO; GO:0016740; F-transferase activity; IEA.

DR GO; GO:0006633; P-fatty acid biosynthesis; IEA.

DR InterPro; IPR01092; Lambda_like_DNA.

DR Pfam; PF03255; ACCTRPRAEA.

DR PRINTS; PRO1069; ACCTRPRAEA.

DR TIGRFAMS; TIGR00513; accA; 1.

KW Complete proteome; Transferase.

SQ SEQUENCE 319 AA; 35699 MW; 31P99366BE2A4667 CRC64;

QY 2 PXRPYXL 8
 ID Q9TUFO | |||
 Db 67 PQRPYTL 73

RESULT 40

Q9JUP0 PRELIMINARY; PRT; 319 AA.

ID Q9TUFO; PRELIMINARY; PRT; 319 AA.

AC Q9TUFO; PRELIMINARY; PRT; 319 AA.

DT 01-OCT-2000 (TREMBLel. 15, Created)

DT 01-OCT-2000 (TREMBLel. 15, Last sequence update)

DT 01-JUN-2003 (TREMBLel. 24, Last annotation update)

DB Putative acetyl-CoA carboxylase carboxyl transferase subunit (BC
6.4.1.2).

GN Name=acCA; OrderedLocusNames=NMA1349;

OS Neisseria meningitidis (serogroup A).

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

OX NCBI_TaxID=65699;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=22491 / Serogroup A / Serotype 4M;

RX MEDLINE=2022556; PubMed=10761919; DOI=10.1038/35006655;

RA Packhill J., Achtnan M., James K.D., Bentley S.D., Churcher C.M.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Churcher C.M.,
RA Davies R.M., Davis P., Devlin K., Fellwell T., Hamlin N., Horoyd S.,
RA Jigels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis 22491.";
RL Nature 404:502-506(2000).

DR IEMI; AU162755; CAB84595; -.

DR PIR; H81901; H81903.

DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.

DR GO; GO:0003939; Facetvl-CoA carboxylase activity; IEA.

DR GO; GO:0016974; F-ligase activity; IEA.

DR GO; GO:0011670; Fatty acid transferase activity; IEA.

DR GO; GO:0006633; P_fatty acid biosynthesis; IEA.

DR InterPro; IPR001095; Ac-CoA_carboxylA.

DR Pfam; PF03255; ACCA; 1.

DR PRINTS; PR01069; ACCCTPFRSEA.

DR TIGRFAM; TIGR00513; accA; 1.

KW Complete proteome; Ligase; Transferase.

SQ SEQUENCE 319 AA; 35492 MW; EA753CDSE169BCB0 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 319;
Best Local Similarity 71.4%; Pred. No. 4.5e-02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPYXL 8
 ID Q9TUFO | |||
 Db 67 PQRPYTL 73

Search completed: March 28, 2005, 08:37:17
Job time : 124 secs

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GenCore version 5.1.6
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OM protein - protein search, using BW model
Run on: March 28, 2005, 08:33:43 ; Search time 39 Seconds
(without alignments)
19.737 Million cell updates/sec

Title: US-10-036-918B-4

Perfect score: 33

Sequence: 1 XPKRPyXL 8

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%, Maximum Match 100%

Listing first 100 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	90.9	360	2 H97447	probable ferredoxin
2	30	90.9	360	2 A12665	ferredoxin I Atu07
3	30	90.9	1100	2 S43677	protein tyrosine k
4	29	87.9	253	1 C47031	orf1_3' of bah - st
5	29	87.9	312	2 A81389	acetyl-CoA carboxy
6	29	87.9	315	2 I64065	acetyl-CoA carboxy
7	29	87.9	316	2 D83192	acetyl-coenzyme A
8	29	87.9	319	1 A43452	acetyl-CoA carboxy
9	29	87.9	319	2 AB0531	acetyl-coenzyme A
10	29	87.9	319	2 H82836	probable acetyl-Co
11	29	87.9	319	2 H81903	acetyl-CoA carboxy
12	29	87.9	319	2 B81119	acetyl-CoA carboxy
13	29	87.9	319	2 C90652	acetyl-CoA carboxy
14	29	87.9	319	2 C85503	acetyl-CoA carboxy
15	29	87.9	319	2 F82100	acetyl-CoA carboxy
16	29	87.9	319	2 AC0130	acetyl-CoA carboxy
17	29	87.9	385	2 A12959	methanesulfonate s
18	29	87.9	385	2 E9832	tachykinin receptor
19	29	87.9	504	2 A41783	prolyl endopeptidase
20	29	87.9	685	2 B75257	ragC protein - Bra
21	29	87.9	1060	2 T31341	protein tyrosine k
22	29	87.9	1099	2 S48053	neurotensin - bovi
23	28	84.8	13	1 UNBO	stringent starvati
24	28	84.8	150	2 D64123	stringent starvati
25	28	84.8	158	2 F82305	stringent starvati
26	28	84.8	165	2 E91141	stringent starvati
27	28	84.8	165	2 JS0666	stringent starvati
28	28	84.8	165	2 H85986	stringent starvati
29	84.8		166	2 ADD0908	stringent starvati

30	28	84.8	169	2 A28146	neurotensin / neuroneotensin precursor
31	28	84.8	170	1 UNDG	probable stringent transcription regu
32	28	84.8	171	2 A10332	transcription regu
33	28	84.8	312	2 F87546	Web/Tag/CpAF fam
34	28	84.8	316	2 F87260	chalcone synthase
35	28	84.8	389	2 T05612	hypothetical prote
36	28	84.8	389	2 T0970	chalcone synthase
37	28	84.8	390	2 T10742	ammonium transport
38	28	84.8	514	2 T05585	urease (EC 3.5.1.5)
39	28	84.8	569	2 S75169	urease (EC 3.5.1.5)
40	28	84.8	569	2 C36350	hypothetical prote
41	27	81.8	141	2 T08790	hypothetical prote
42	27	81.8	161	2 H82696	hypothetical prote
43	27	81.8	175	2 T26604	hypothetical prote
44	27	81.8	246	2 T30490	hypothetical prote
45	27	81.8	312	2 F71922	acetyl-CoA carboxy
46	27	81.8	312	2 E65589	flavohemoprotein [
47	27	81.8	378	2 AF3320	aspartic proteinases
48	27	81.8	420	2 T06000	hypothetical prote
49	27	81.8	430	2 G83110	hypothetical prote
50	27	81.8	570	2 AF3558	urease (EC 3.5.1.5)
51	27	81.8	570	2 S28509	probable phosphoen
52	27	81.8	576	2 C56613	hypothetical prote
53	27	81.8	569	2 A97648	cell proliferation
54	27	81.8	569	2 AG2871	urease alpha subun
55	27	81.8	570	2 S42607	urease (EC 3.5.1.5)
56	27	81.8	570	2 E72754	urease - Old W
57	27	81.8	622	2 T32939	virion morphogene
58	27	81.8	2938	2 T30549	conserved hypothet
59	26	78.8	79	2 B84400	ribonuclease XE261
60	26	78.8	129	2 S48814	hypothetical prote
61	26	78.8	154	2 S48101	hypothetical prote
62	26	78.8	156	2 A83240	xyloglucan endo-1,
63	26	78.8	161	2 T10392	hypothetical prote
64	26	78.8	173	2 H82335	probable N-acetylm
65	26	78.8	174	2 B77453	extensin (clone Ex
66	26	78.8	197	2 E97501	conserved hypothet
67	26	78.8	190	2 A83240	cysteine-rich Secr
68	26	78.8	209	2 T03338	hypothetical prote
69	26	78.8	211	2 C75836	hypothetical prote
70	26	78.8	212	2 T03338	hypothetical prote
71	26	78.8	224	2 G7014	hypothetical prote
72	26	78.8	227	2 B49202	hypothetical prote
73	26	78.8	241	2 C36308	hypothetical prote
74	26	78.8	253	2 A55652	Oct-binding factor
75	26	78.8	256	2 AB1652	phage related prot
76	26	78.8	260	2 A11587	phage related prot
77	26	78.8	260	2 AC1198	conserved hypothet
78	26	78.8	268	2 E72808	gp69 protein - Myc
79	26	78.8	269	2 T02336	extensin precursor
80	26	78.8	280	2 T48975	xyloglucan endo-tr
81	26	78.8	293	2 S48102	xyloglucan endo-1,
82	26	78.8	295	2 T49148	hypothetical prote
83	26	78.8	300	2 AB3431	hydroxycycloglutath
84	26	78.8	305	2 H81557	conserved hypothet
85	26	78.8	316	2 H86509	CT149 hypothetical
86	26	78.8	316	2 B72113	MM-1 cell derived
87	26	78.8	318	2 JE0284	hypothetical prote
88	26	78.8	325	2 T33220	hypothetical prote
89	26	78.8	325	2 C95952	hypothetical prote
90	26	78.8	325	2 B81694	probable UDP gluco
91	26	78.8	354	2 D71539	UDP-3-O-(R-3-hydro
92	26	78.8	360	2 F72094	UDP-3-O-(R-3-hydro
93	26	78.8	360	2 F86528	UDP glucosamine N-
94	26	78.8	361	2 S48053	probable phosphino
95	26	78.8	361	2 A24248	inhibin alpha chain
96	26	78.8	365	2 T04372	neurotensin / neur
97	26	78.8	390	1 TVIWG	neurotensin / neur
98	26	78.8	408	2 G8306	probable stringen
99	26	78.8	410	2 T06213	probable stringen
100	26	78.8	410	2 T04372	probable stringen

ALIGNMENTS

RESULT 1

A;Title: Genome sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens (strain C58, Cereon) - Agrobacterium tumefaciens (strain C58, Cereon)
 C;Species: Agrobacterium tumefaciens
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C;Accession: H97447
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A;Reference number: A97359; MUID:21608551; PMID:11743194
 A;Accession: H97447
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-360 <KUR>
 A;Cross-references: UNIPROT:Q8UHFS; GB:AE007869; PIDN:AABK86537.1; PID:91515697; GSPDB:G
 C;Genetics:
 A;Gene: AGR_C_1321
 A;Map position: circular chromosome
 C;Superfamily: phthalate dioxygenase reductase; cytochrome-b5 reductase homology;ferred

RESULT 2

Query Match 90.9%; Score 30; DB 2; Length 360;
 Best Local Similarity 71.4%; Pred. No. 48; Mismatches 5; Conservative 0; Indels 0; Gaps 0;
 Matches 2;| | | | |
 Qy 2 PXPYXXL 8
 Db 77 PSRPyAL 83

RESULT 4

Query Match 90.9%; Score 30; DB 2; Length 1100;
 Best Local Similarity 71.4%; Pred. No. 1.6e+02; Mismatches 5; Conservative 0; Indels 0; Gaps 0;
 Matches 2;| | | | |
 Qy 2 PXPYXXL 8
 Db 228 PSRPyAL 234

RESULT 5

Query Match 87.9%; Score 29; DB 1; Length 253;
 Best Local Similarity 71.4%; Pred. No. 54; Mismatches 5; Conservative 0; Indels 0; Gaps 0;
 Matches 2;| | | | |
 Qy 2 PXPYXXL 8
 Db 78 PXPYVYL 84

A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: AB2665
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-360 <KUR>
 A;Cross-references: UNIPROT:Q8UHFS; GB:AE008688; PIDN:AAU41743.1; PID:917739094; GSPDB:G
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atu0727
 A;Map position: circular chromosome
 C;Superfamily: Phthalate dioxygenase reductase; cytochrome-b5 reductase homology;ferred

Query Match 90.9%; Score 30; DB 2; Length 360;
 Best Local Similarity 71.4%; Pred. No. 48; Mismatches 5; Conservative 0; Indels 0; Gaps 0;
 Matches 2;| | | | |
 Qy 2 PXPYXXL 8
 Db 77 PSRPyAL 83

RESULT 3

S43677 protein tyrosine kinase JAK3 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004
 C;Accession: S43677

R;Takahashi, T.; Shirasawa, T.
 FEBS Lett. 342, 124-128, 1994
 A;Title: Molecular cloning of rat JAK3, a novel member of the JAK family of protein tyrosine kinases
 A;Reference number: S43677; MUID:94192816; PMID:8143863
 A;Accession: S43677
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1100 <PAK>
 A;Cross-references: UNIPROT:Q63272; GB:D28508; NID:9485811; PIDN:BAA05868.1; PID:di1006416
 C;Superfamily: protein kinase homology
 C;Keywords: ATP
 F515-180/Domain: protein kinase homology <KIN1>
 F,815-1094/Domain: protein kinase homology <KIN2>
 Query Match 90.9%; Score 30; DB 2; Length 1100;
 Best Local Similarity 71.4%; Pred. No. 1.6e+02; Mismatches 5; Conservative 0; Indels 0; Gaps 0;
 Matches 2;| | | | |
 Qy 2 PXPYXXL 8
 Db 228 PSRPyAL 234

RESULT 4

Query Match 90.9%; Score 30; DB 2; Length 1100;
 Best Local Similarity 71.4%; Pred. No. 1.6e+02; Mismatches 5; Conservative 0; Indels 0; Gaps 0;
 Matches 2;| | | | |
 Qy 2 PXPYXXL 8
 Db 228 PSRPyAL 234

RESULT 5

Query Match 87.9%; Score 29; DB 1; Length 253;
 Best Local Similarity 71.4%; Pred. No. 54; Mismatches 5; Conservative 0; Indels 0; Gaps 0;
 Matches 2;| | | | |
 Qy 2 PXPYXXL 8
 Db 78 PXPYVYL 84

A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: AB2665
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-360 <KUR>
 A;Cross-references: UNIPROT:Q8UHFS; GB:AE008688; PIDN:AAU41743.1; PID:917739094; GSPDB:G
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atu0727
 A;Map position: circular chromosome
 C;Superfamily: Phthalate dioxygenase reductase; cytochrome-b5 reductase homology;ferred

Query Match 90.9%; Score 30; DB 2; Length 360;
 Best Local Similarity 71.4%; Pred. No. 48; Mismatches 5; Conservative 0; Indels 0; Gaps 0;
 Matches 2;| | | | |
 Qy 2 PXPYXXL 8
 Db 77 PSRPyAL 83

RESULT 3

S43677 protein tyrosine kinase JAK3 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004
 C;Accession: S43677

Query Match 87.9%; Score 29; DB 2; Length 312;
 Best Local Similarity 71.4%; Pred. No. 68;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 60 PDRPyAL 66

RESULT 6

I4065 acetyl-CoA carboxylase (EC 6.4.1.2), carboxyltransferase alpha chain - *Haemophilus influenzae*
 C;Species: *Haemophilus influenzae*
 C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
 C;Accession: I64065
 R;Pleischmann, M.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gooley, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, D.M.; Brandom, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geohagen, N.S.M.; Science 269, 496-512, 1995
 A;Authors: Ghebre, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Reference number: A64000; MUID:95350630; PMID:7542800
 A;Accession: I64065
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-315 <TIGR>
 A;Cross-references: UNIPROT:P43872; GB:U32724; GB:L4203; NID:91573378; PIDN: AAC22065.1;
 C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain
 A;Accession: 1-315 <BLAT>
 Query Match 87.9%; Score 29; DB 2; Length 315;
 Best Local Similarity 71.4%; Pred. No. 68;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 66 PNRPyTL 72

RESULT 7

D33192 acetyl-coenzyme A carboxyl transferase (alpha subunit) PA3639 [imported] - E
 C;Species: *Pseudomonas aeruginosa*
 C;Accession: D83192
 R;Stover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Beck, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.; Nature 406, 959-964, 2000
 A;Reference number: AB2950; MUID:20437337; PMID:10984043
 A;Accession: D83192
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-316 <STO>
 A;Cross-references: UNIPROT:Q9HXZ2; GB:AE004783; GB:AE004091; NID:59949786; PIDN: AAG0702
 A;Experimental source: strain PA01
 C;Genes: accA; PA3639
 C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain
 Query Match 87.9%; Score 29; DB 2; Length 316;
 Best Local Similarity 71.4%; Pred. No. 68;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 67 PKRPyTL 73

RESULT 8

A43452

RESULT 9

AB0531 acetyl-coenzyme A carboxylase carboxyl transferase chain alpha [imported] - *Salmonella enterica*
 C;Species: *Salmonella enterica* subsp. *enterica* serovar *Typhi*
 A;Note: this species has also been called *Salmonella typhi*
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AB0531
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, Th., T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Barrall, S.; Moule, S.; O'Gara, P.; Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AB0531
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-319 <PAR>	A;Cross-references: GB:AL1513382; PIDN:CAD08690.1; PID:g16501513; GSPDB:GN001176
A;Cross-references:	A;Experimental source: serogroup A, strain 22491
C;Genetics:	
A;Gene: STY0255	A;Gene: accA; NM11349
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain	C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain
Query Match	Query Match
Best Local Similarity 87.9%; Pred. No. 69; Length 319;	Best Local Similarity 87.9%; Pred. No. 69; Length 319;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPyXL 8	Qy 2 PXRPyXL 8
Db 70 PQRPYTL 76	Db 67 PQRPYTL 73
RESULT 10	RESULT 12
H82836 acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha xf0203 [imported] - Xyl	B81119 acetyl-CoA carboxylase, carboxyl transferase alpha chain NMB1139, NMB1177 [imported] - Ne
C;Species: Xylella fastidiosa	C;Species: Neisseria meningitidis
C;Accession: H82836	C;Accession: 31-Mar-2000 #Sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
N;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen	R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
A;Title: The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> .	Hickey, E.K.; Hatt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
A;Reference number: AB2515; MUID:20365717; PMID:10910347	Hu, H.; Qin, H.; Yamashita, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizzini, M.
A;Note: for a complete list of authors see reference number A59328 below	Science 287, 1809-1815, 2000
A;Accession: H82836	A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A;Status: preliminary	A;Title: Complete genome sequence of <i>Neisseria meningitidis</i> serogroup B strain MC58.
A;Molecule type: DNA	A;Reference number: AB1000; MUID:20175755; PMID:10710307
A;Residues: 1-319 <SIM>	A;Molecule type: DNA
A;Experimental source: strain 945C	A;Residues: 1-319 <TER>
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aceacio, M.; Alvarenga, R.; A	A;Cross-references: UNIPROT:Q9URV8; GB:AE002462; GB:AE002098; NID:97226363; PIDN:AAF4152;
Briones, M.R.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H	A;Experimental source: serogroup B, strain MC58
submitted to GenBank, June 2000	A;Accession: G81114
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Pragia, J.S.; Franca, S.C.; Franco, M.C.; Probst	A;Molecule type: DNA
J.D.; Tunquera, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig	A;Residues: 1-319 <TER>
chado, M.R.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E	A;Cross-references: GB:AB002465; GB:AE002098; NID:97226401; PIDN:AAF41562.1; PID:97226414
A;Authors: Martins, E.M.F.; Matsukawa, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; A	A;Experimental source: serogroup B, strain MC58
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmeiro, D.A.	C;Genetics:
Rodrigues, V.; Rose, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawaka	A;Gene: NMB1139; NMB1177
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva Jr., W.A.; da Silva, M.	C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain
M.; Tsunaka, M.H.; Vallada, H.; van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; 2	Query Match
A;Reference number: A59328	Best Local Similarity 87.9%; Pred. No. 69; Length 319;
A;Contents: annotation	Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
C;Genetics:	Qy 2 PXRPyXL 8
A;Gene: XF0203	Db 67 PQRPYTL 73
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain	RESULT 13
Query Match	C90652 acetyl-CoA carboxylase (EC 6.4.1.2) carboxyltransferase alpha chain - Escherichia coli (E
Best Local Similarity 87.9%; Pred. No. 69;	C;Species: Escherichia coli
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	C;Accession: 18-Jun-2001 #Sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
Qy 2 PXRPyXL 8	C;Accession: C90652
Db 67 PQRPYTL 73	R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.,
RESULT 11	gakawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
H81903 probable acetyl-CoA carboxylase (EC 6.4.1.2) carboxyltransferase alpha chain NMA1349 [si	A;Residues: 1-319 <DNA>
C;Species: Neisseria meningitidis	A;Cross-references: UNIPROT:P30067; GB:BA000007; PIDN:BA033610.1; PID:g133359643; GSPDB:GN
C;Accession: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004	A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Accession: H81903	C;Genetics:
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel	A;Accession: AB9629; MUID:21156231; PMID:11258796
; Hollroyd, S.; Jolley, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,	A;Status: preliminary
Nature 404, 502-505, 2000	A;Molecule type: DNA
A;Title: Complete DNA sequence of a serogroup A strain of <i>Neisseria meningitidis</i> Z2491.	A;Residues: 1-319 <DNA>
A;Reference number: A81775; MUID:20222556; PMID:10761919	A;Cross-references: UNIPROT:P30067; GB:BA000007; PIDN:BA033610.1; PID:g133359643; GSPDB:GN
A;Accession: H81903	A;Experimental source: strain O157:H7, substrain RIMD 0509952
A;Status: preliminary	C;Genetics:
A;Molecule type: DNA	A;Gene: EC0187
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain	

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
Db 70 PQRPYTL 76

RESULT 14

C05503 acetyl-CoA carboxylase (EC 6.4.1.2) carboxyltransferase alpha chain [similarity] - Esche

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: C05503
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimantova, E.; Potamouidis, K.; Apodaca, A.;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: C05503

A;Molecule type: DNA

A;Residues: 1-319 <STO>

A;Cross-references: UNIPROT:P30867; GB:AE005174; NID:912512913; PIDN:AA654487.1; GSPDB:G

A;Experimental source: strain O157:H7, substrain EDL933

A;Genetics: C;Gene: accA

C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;
Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
Db 70 PQRPYTL 76

RESULT 15

F82100 acetyl-CoA carboxyl transferase alpha chain VC2244 [imported] - Vibrio chol

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: F82100
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Brzuska, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.; Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20400833; PMID:10953301

A;Accession: F82100

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-319 <HEI>

A;Cross-references: UNIPROT:Q9KPM8; GB:AE004296; DB:AE003852; NID:99656799; PIDN:AAF9538

A;Experimental source: seroGroup Oil; strain N1651; biotype El Tor

A;Gene: VC2244

A;Map position: 1
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain

Query Match 87.9%; Score 29; DB 2; Length 319;
Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

RESULT 16

AC0130. acetyl-CoA carboxylase (EC 6.4.1.2) alpha chain [imported] - Yersinia pestis (strain CG9;

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C;Accession: AC0130

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, P.; Dougan, G.; Feltwell, T.; Hedges, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Goodwin, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, R.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB00001; MUID:21470413; PMID:11586360

A;Accession: AC0130

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-319 <KUR>

A;Cross-references: UNIPROT:Q8ZHS2; GB:AL590842; PIDN:CA89902.1; PID:gi15979127; GSPDB:G

A;Gene: accA

C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;
Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

RESULT 17

A12959 methanesulfonate sulfonatase Atu3279 [imported] - Agrobacterium tumefaciens (strain C58,

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C;Accession: A12959

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monk, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; erge, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClelland, J.; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.; Bter, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: A12959

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-385 <KUR>

A;Cross-references: UNIPROT:Q8UW18; GB:AE008689; PIDN:AAL44095.1; PID:gi17741662; GSPDB:G

A;Experimental source: strain C58 (Dupont)

A;Genetics: C;Gene: Atu3279

A;Map position: linear chromosome

Query Match 87.9%; Score 29; DB 2; Length 385;
Best Local Similarity 71.4%; Pred. No. 85; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 171 PARPyQL 177

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;

Best Local Similarity 71.4%; Pred. No. 69; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8

Db 70 PQRPYTL 76

C;Keywords: ligase

Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens C58, Strain R5951; PMID:11743194
A;Reference number: A97359; MUID:21608551; PIDN:CAA12353.1; PID:921
A;Accession: E98323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-385 <KUR>
A;Cross-references: UNIPROT:Q8UAT8; GB:AE007870; PIDN:AAK90111.1; PID:915160102; GSPDB:G
C;Genetics:
A;Gene: AGR_L_3078
A;Map position: linear chromosome

RESULT 19
Query Match 87.9%; Score 29; DB 2; Length 385;
Best Local Similarity 71.4%; Pred. No. 85; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
Db 171 PAPYQL 177

RESULT 19
tachykinin receptor NKD - fruit fly (*Drosophila melanogaster*)
C;Species: *Drosophila melanogaster*
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
C;Accession: A41783
R;Monnier, D.; Colas, J.-F.; Rosay, P.; Hen, R.; Borrelli, E.; Marteaux, L.
J. Biol. Chem. 267, 1288-1302, 1992
A;Title: NKD, a developmentally regulated tachykinin receptor in *Drosophila*.
A;Reference number: A41783; MUID:92112776; PMID:1370464
A;Accession: A41783
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-504 <MON>
A;Note: Sequence extracted from NCBI backbone (NCBIP:76545)
C;Genetics:
A;Gene: FlyBase:Takr86C
A;Cross-references: FlyBase:FBgn0004841
C;Superfamily: neuropeptin 1 receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 87.9%; Score 29; DB 2; Length 504;
Best Local Similarity 71.4%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
Db 72 PTRPyEL 78

RESULT 20
prolyl endopeptidase - *Deinococcus radiodurans* (strain R1)
C;Species: *Deinococcus radiodurans*
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: B75267
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Mau, M.; Shem, M.; Vaishnav, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A;Accession: B75267
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-686 <WHT>
A;Cross-references: EMBL:U2955
R;Mittmann, B.A.; Silvennoinen, O.; Miura, O.; Lai, K.S.; Cwik, C.; Liu, E.T.; Ihle, J.N.
A;Reference number: S51607
A;Accession: S51607
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-61, A'-62-1099 <WT2>
A;Cross-references: EMBL:U2955; NID:9529238; PIDN:AAA21565.1; PID:9529239
C;Supfamily: protein kinase homology
C;Keywords: ATP
F;914-779/Domain: protein kinase homology <KIN1>
F;915-1093/Domain: protein kinase homology <KIN2>
F;824-832/Region: protein kinase ATP-binding motif

Query Match 87.9%; Score 29; DB 2; Length 1099;
Best Local Similarity 71.4%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
Db 396 PSRPyRL 402

RESULT 21
T31341
rgc protein - *Bradyrhizobium japonicum*
C;Species: *Bradyrhizobium japonicum*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31341
R;Narberhaus, F.; Krummenacher, P.; Fischer, H.M.; Hennecke, H.
Mol. Microbiol. 24, 931-104, 1997
A;Title: Three disparately regulated genes for sigma32-like transcription factors in Bracillus
A;Reference number: 221007; MUID:97285751; PMID:9140968
A;Accession: T31341
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1060 <WAK>
A;Cross-references: UNIPROT:O69238; EMBL:AU225023; NID:92961292; PIDN:CAA12353.1; PID:921
C;Genetics:
A;Gene: rggC
C;Accession: A41783
C;Superfamily: cation efflux system membrane protein czcA
Query Match 87.9%; Score 29; DB 2; Length 1060;
Best Local Similarity 71.4%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
Db 615 PAPYNL 621

RESULT 22
S48053
protein tyrosine kinase - mouse
C;Species: *Mus musculus* (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 16-Aug-2004
C;Accession: S48053; MUID:551607
R;Mittmann, B.A.; Silvennoinen, O.; Miura, O.; Lai, K.S.; Cwik, C.; Liu, E.T.; Ihle, J.N.
Nature 370, 153-157, 1994
A;Title: Involvement of the Jak-3 Janus kinase in signalling by interleukins 2 and 4 in T cells
A;Reference number: S48053; MUID:94294024; PMID:8022486
A;Accession: S48053
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1099 <WT>
A;Cross-references: EMBL:U2955
R;Mittmann, B.A.; Silvennoinen, O.; Miura, O.; Lai, K.S.; Cwik, C.; Liu, E.T.; Ihle, J.N.
A;Reference number: S51607
A;Accession: S51607
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-61, A'-62-1099 <WT2>
A;Cross-references: EMBL:U2955; NID:9529238; PIDN:AAA21565.1; PID:9529239
C;Supfamily: protein kinase homology
C;Keywords: ATP
F;914-779/Domain: protein kinase homology <KIN1>
F;915-1093/Domain: protein kinase homology <KIN2>
F;824-832/Region: protein kinase ATP-binding motif

Query Match 87.9%; Score 29; DB 2; Length 1099;
Best Local Similarity 71.4%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
Db 72 PTRPyEL 78

Db 228 PGRPYAL 234
R;Heidelberg, J.F.; Ebsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
charlson, D.; Emiliaeva, M.D.; Yarmatseva, J.; Basz, S.; Qin, H.; Dragoi, I.; Sellers, P.
C;Species: Bos primigenius taurus (cattle)
C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 24-Feb-1995
C;Accession: A01420
R;Carraway, R.; Leeman, S.E.
J. Biol. Chem. 250, 1907-1911, 1975
A;Title: The amino acid sequence of a hypothalamic peptide, neurotensin.
A;Reference number: A92172; MUID:75095678; PMID:1167549
A;Accession: A01420
A;Molecule type: protein
A;Residues: 1-13 <CAR>
A;Experimental source: hypothalamus
R;Carraway, R.; Leeman, S.E.
J. Biol. Chem. 250, 1912-1918, 1975
A;Title: The synthesis of neurotensin.
A;Reference number: A92173; MUID:75095679; PMID:1112838
A;Contents: annotation; Synthesis
A;Note: a tridecapeptide chemically and pharmacologically identical with the natural peptide
C;Keywords: neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidine carboxylic acid (Gln) #status experimental

Query Match 84.8%; Score 28; DB 1; Length 13;
Best Local Similarity 71.4%; Pred. No. 3.7;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PXRPyXL 8
Db 7 PRPpYL 13

RESULT 24
D64123
stringent starvation protein sspB - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 12-Jul-2004
C;Accession: D64123
R;Pleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weilman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995
A;Authors: Graham, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: D64123
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-150 <TIGR>
A;Cross-references: UNIPROT:P45206; GB:U32822; GB:L42023; NID:91574265; PIDN: AAC23089.1; C;Gene: sspB
C;Superfamily: Clpx-specific adaptor protein sspB

Query Match 84.8%; Score 28; DB 2; Length 150;
Best Local Similarity 71.4%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PXRPyXL 8
Db 7 PRPpYL 13

RESULT 25
F82305
stringent starvation protein B vc0577 [imported] - Vibrio cholerae (strain N16961 serogr C;Species: Vibrio cholerae
C;Accession: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 12-Jul-2004
C;Accession: F82305

Query Match 84.8%; Score 28; DB 2; Length 150;
Best Local Similarity 71.4%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PXRPyXL 8
Db 7 PRPpYL 13

RESULT 26
E91141
stringent starvation protein B [imported] - Escherichia coli (strain O157:H7, substrain F)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 12-Jul-2004
C;Accession: E91141
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G., Gabawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E91141
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-165 <HAY>
A;Experimental source: strain O157:H7, substrain RIMD 0509952
A;Cross-references: UNIPROT:P25663; GB:BA000007; PIDN:BAB37524.1; PID:913363574; GSPDB:GN C;Genetics: L.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
C;Superfamily: Clpx-specific adaptor protein SspB

Query Match 84.8%; Score 28; DB 2; Length 165;
Best Local Similarity 71.4%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PXRPyXL 8
Db 8 PRPpYL 14

RESULT 27
JS0666
stringent starvation protein B, sspB - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 12-Jul-2004
C;Accession: JS0666; FF5114
R;Williams, M.D.; Fuchs, A.; Flickinger, M.C.
Gene 109, 21-30, 1991
A;Title: Null mutation in the stringent starvation protein of Escherichia coli disrupts 11 A;Reference number: JS0666; MUID:92057948; PMID:1721886
A;Accession: JS0666
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-165 <WIL>
A;Cross-references: UNIPROT:P25663; GB:MB6028; NID:9147871; PIDN:AAA24650.1; PID:9147872
R;Blattner, R.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cole, J.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of *Escherichia coli* K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F65114
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-165 <BLAT>
A;Cross-references: GB:AE000402; GB:U00096; NID:G1789619; PIDN: AAC76260.1; PID:g1789623;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: sspB
C;Superfamily: CIPX-specific adaptor protein SspB

RESULT 28

Query Match 84.8%; Score 28; DB 2; Length 165;
Best Local Similarity 71.4%; Pred. No. 56; Mismatches 5; Conservative 0; Indels 0; Gaps 0;
Matches 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXKPYXL 8
Db 8 PRRPYLL 14

RESULT 29

stringent starvation protein B [imported] - *Escherichia coli* (strain 0157:H7, substrain H85986
C;Species: *Escherichia coli*
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 12-Jul-2004
C;Accession: H85986
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, E.J.; Davis, N.W.; Lin, A.; Dimaranta, E.; Potamitis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85986
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-165 <STO>
A;Cross-references: UNIPROT:P25563; GB:AE005174; NID:g12517846; PIDN: AAG58356.1; GSPDB:G
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: sspB
C;Superfamily: CIPX-specific adaptor protein SspB

Query Match 84.8%; Score 28; DB 2; Length 165;
Best Local Similarity 71.4%; Pred. No. 56; Mismatches 5; Conservative 0; Indels 2; Gaps 0;
Matches 5; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PXKPYXL 8
Db 8 PRRPYLL 14

RESULT 30

A8146
neurotensin / neuromedin N precursor - rat
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: A8146; A56789
R;Kislauksis, E.; Bullock, B.; McNeill, S.; Dobner, P.R. J. Biol. Chem. 263, 4963-4968, 1988
A;Title: The rat gene encoding neurotensin and neuromedin N. Structure, tissue-specific expression and primary structure
A;Reference number: A28146; MUID:88169625; PMID:2832414
A;Accession: A28146
A;Molecule type: mRNA
A;Residues: 1-169 <KUS>
A;Cross-references: UNIPROT:P24068
R;Bidard, J.N.; de Nadai, F.; Rovere, C.; Moinier, D.; Laur, J.; Martinez, J.; Cuber, J.C. Biochem. J. 291, 225-233, 1993
A;Title: Immunological and biochemical characterisation of processing products from the rat neurotensin gene
A;Accession: A56789
A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-42 <BDI>
A;Experimental source: medullary thyroid carcinoma 6-23 cell extracts
A;Note: sequence extracted from NCBI backbone (NCBIP:129397)
C;Superfamily: neurotensin
C;Keywords: neuropeptide

Query Match 84.8%; Score 28; DB 2; Length 169;
Best Local Similarity 71.4%; Pred. No. 58; Mismatches 5; Conservative 0; Indels 2; Gaps 0;
Matches 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXKPYXL 8
Db 156 PRRPYIL 162

RESULT 31

UNPQ
neurotensin precursor - dog
N;Contains: neuropeptid N; neuropeptid N-125; neuropeptid N-126
C;Species: *Canis lupus familiaris* (dog)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A28025; B60319; AA0319; A60324; JN0293; A16272
R;Dobner, P.R.; Barber, D.L.; Villa-Komaroff, L.; McKiernan, C. Proc. Natl. Acad. Sci. U.S.A. 84, 3516-3520, 1987
A;Title: Cloning and sequence analysis of cDNA for the canine neuropeptid N-126
A;Reference number: A28025; MUID:87204168; PMID:3472221
A;Accession: A28025
A;Molecule type: mRNA
A;Residues: 1-170 <DOS>
A;Cross-references: UNIPROT:P10673; GB:MI6443; NID:9164033; PIDN: AAA30878.1; PID:g164034
R;Mitra, S.P.; Muraki, K.; Brown, D.R.; Parsons, A.M.; Caraway, R.E. Regul. Pept. 28, 11-22, 1990
A;Title: Canine neuropeptid N-126 and neuropeptid N-125
A;Reference number: A60319; MUID:9022594; PMID:2158127
A;Accession: B60319
A;Molecule type: protein
A;Residues: 14-14 <MT>
A;Accession: A60319
A;Molecule type: protein
A;Residues: 'E', 152-163 <MT2>
R;Nogard, M.H.; Reeve Jr., J.R.; Shively, J.B.; Ben-Avram, C.M.; Bysselin, V.E.; Walsh, C;Genetics:
A;Gene: STY3522

Regul. Pept. 14, 313-321, 1986
 A;Pittle: Isolation and characterization of a neurotensin-like decapeptide from a canine
 A;Reference number: A60324; MUID:86314883; PMID:3749527
 A;Accession: A60324
 A;Molecule type: protein
 A;Residue: 154-163 <MOD>
 R;Carraway, R.B.; Mitra, S.P.
 Bloch. Biophys. Res. Commun. 179, 301-308, 1991
 A;Title: Purification of large neuropeptides from canine intestine and its identity
 A;Reference number: JN1293; MUID:91354266; PMID:1883359
 A;Accession: JN1293
 A;Molecule type: protein
 A;Residues: 24-43 <CAR>
 A;Experimental source: small intestine
 R;Carraway, R.B.; Mitra, S.P.
 J. Biol. Chem. 265, 8627-8631, 1990
 A;Title: Differential processing of neuropeptides from canine intestine and its identity
 A;Reference number: A36272; MUID:90256783; PMID:2343398
 A;Accession: A36272
 A;Molecule type: protein
 A;Residues: 128-147 <CH2>
 C;Superfamily: neurotensin
 C;Keywords: hormone; neuropeptide; pyroglutamic acid
 F-1-23/Domain: signal sequence #status predicted <SIG>
 F-24-148/Product: large neuropeptides #status experimental <NM>
 F-143-148/Product: neuropeptides #status experimental <NTS>
 F-151-163/Product: neuropeptides #status experimental <NTM>
 F-151/Modified site: pyrrolidine carboxylic acid (Gln) (in mature form) #status experimental <NM>
 Query Match 84.8%; Score 28; DB 1; Length 170;
 Best Local Similarity 71.4%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 2;
 Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 157 PRRPPTL 163

RESULT 32

A10432 probable stringent starvation protein B sspB [imported] - Yersinia pestis (strain C092)
 C;Species: Yersinia pestis
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 12-Jul-2004
 C;Accession: A10432
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Rutter, J.; Embley, M.; White, S.L.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Nature 413, 523-527, 2001
 A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:11586360
 A;Accession: A10432
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-171 <KUR>
 A;Cross-references: UNIPROT:Q9ABX5; GB:AL590842; PIDN:CAC92789.1; PID:g15981482; GSPDB:G
 C;Genetics:
 A;Gene: sspB
 C;Superfamily: Clpx-specific adaptor protein SspB

Query Match 84.8%; Score 28; DB 2; Length 316;
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 2;
 Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 28 PRRPPTL 34

RESULT 33

F87546
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonay, N.J.; Embley, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Proc. Natl. Acad. Sci. U.S.A. 98, 4156-4161, 2001
 A;Title: Complete Genome Sequence of *Caulobacter crescentus*.
 A;Reference number: AB7249; MUID:21173698; PMID:11259647
 A;Accession: F87546
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-312 <STD>
 C;Genetics:
 A;Gene: CC0095
 C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C;Accession: F87260
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonay, N.J.; Embley, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of *Caulobacter crescentus*.
 A;Reference number: AB7249; MUID:21173698; PMID:11259647
 A;Accession: F87260
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-316 <STD>
 A;Cross-references: UNIPROT:Q9ABX5; GB:AE005673; NID:g13421198; PIDN:AAK22082.1; GSPDB:G
 A;Gene: CC0095

Query Match 84.8%; Score 28; DB 2; Length 316;
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 2;
 Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 28 PRRPPTL 34

RESULT 34

F87260
 WebTAG/CPSF family protein [imported] - *Caulobacter crescentus*
 C;Species: *Caulobacter crescentus*
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C;Accession: F87260
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonay, N.J.; Embley, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of *Caulobacter crescentus*.
 A;Reference number: AB7249; MUID:21173698; PMID:11259647
 A;Accession: F87260
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-312 <STD>
 C;Genetics:
 A;Gene: CC0095
 C;Species: *Oryza sativa* (rice)
 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 15-Mar-2004
 C;Accession: T03612
 R;Zhang, Y.; Qu, L.; Xie, M.; Gu, H.; Chen, Z. submitted to the EMBL Data Library, September 1995
 A;Description: cDNA sequence of a CHS-like gene from rice flower.
 A;Reference number: Z14978
 A;Accession: T03612
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-389 <ZHA>
 A;Cross-references: EMBL:X91811; NID:g1009983; PID:g1008984
 A;Experimental source: cv. Zhonghua 10
 C;Genetics:
 A;Gene: chslk
 C;Superfamily: Type III polyketide synthase

RESULT 33

F87546
 transcription regulator, AraC family [imported] - *Caulobacter crescentus*
 C;Species: *Caulobacter crescentus*
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

Query Match 84.8%; Score 28; DB 2; Length 389;
 Best Local Similarity 71.4%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 209 PDRPyDL 215

RESULT 36

T02970 Hypothetical protein YW2 - rice
 C;Species: Oryza sativa (rice)
 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
 C;Accession: T02970
 R:Hihara, Y.; Hara, C.; Uchimiyama, H.
 Plant Mol. Biol. 30, 1181-1193, 1996
 A;Title: Isolation and characterization of two cDNA clones for mRNAs that are abundantly
 A;Reference number: Z14800; MUID:96311007; PMID:8704128
 A;Accession: T02970
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-389 <HII>
 A;Cross-references: UNIPROT:023811; EMBL:D50576; NID:92645169; PIDN:BAA23618_1; PID:9264
 A;Experimental source: another, cultivar Hayayuki
 C;Superfamily: Type III polyketide synthase

Query Match 84.8%; Score 28; DB 2; Length 389;
 Best Local Similarity 71.4%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 209 PDRPyDL 215

RESULT 37

T10742 Chalcone synthase homolog Chs1 - Monterey pine
 C;Species: Pinus radiata (Monterey pine)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Mar-2004
 C;Accession: T10742
 R:Wallden, A.R.; Walter, C.; Gardner, R.C.
 submitted to the EMBL Data Library, February 1997
 A;Description: Genes expressed in pinus radiata male cones.
 A;Reference number: Z17111
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-390 <WAL>
 A;Cross-references: EMBL:U90341; NID:92507616; PID:92507617
 A;Experimental source: strain 880/607; tissue_type male cone; clone PAW192
 C;Superfamily: Type III polyketide synthase

Query Match 84.8%; Score 28; DB 2; Length 390;
 Best Local Similarity 71.4%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 209 PERPYDL 215

RESULT 38

T06585 Ammonium transporter 2 - tomato
 C;Species: Lycopersicon esculentum (tomato)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T06585
 R:Lauter, F.R.; Nurnmann, O.; Frommer, W.B.
 submitted to the EMBL Data Library, January 1996
 A;Description: Cloning and characterization of the ammonium transporter LeAMT2 from toma
 A;Reference number: Z15776

Query Match 84.8%; Score 28; DB 2; Length 514;
 Best Local Similarity 71.4%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 409 PNRPYGL 415

RESULT 39

S75169 urease (EC 3.5.1.5) alpha chain - Synechocystis sp. (strain PCC 6803)
 N;Alternate names: Protein sll1750
 C;Species: Synechocystis sp.

A;Variety: PCC 6803
 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C;Accession: S75169
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanebe, A.; Yamada, M.; Yasuda,
 DNA Res. 3, 109-136, 1996
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 A;Reference number: S74322; MUID:97061201; PMID:8905231
 A;Accession: S75169
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-569 <KAN>
 A;Cross-references: UNIPROT:P773061; EMBL:D90903; GB:AB001339; NID:91652127; PIDN:BAA1708;
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C;Genetics:
 A;Gene: ureC
 C;Superfamily: urease, alpha subunit; urease 62K chain homology
 C;Keywords: hydrolase; metalloprotein; nickel
 P5-552;Domain: urease 62K chain homology <U62>
 P;136,138,219,362/Binding site: nickel 2 (His, His, Lys, ASP) #status predicted

Query Match 84.8%; Score 28; DB 2; Length 569;
 Best Local Similarity 57.1%; Pred. No. 2.1e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 302 PTRPYTI 308

RESULT 40

C36950 Uracil chain - Bacillus sp. (strain TB-90)
 C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 16-Aug-2004
 N;Alternate names: urcC protein
 C;Species: Bacillus sp.
 C;Accession: C36950
 R;Maeda, M.; Hidaka, M.; Nakamura, A.; Masaki, H.; Uozumi, T.
 J. Bacteriol. 176, 433-442, 1994
 A;Title: Cloning, sequencing, and expression of thermophilic Bacillus sp. strain TB-90 ur
 A;Reference number: A36950; MUID:94117379; PMID:8288539
 A;Accession: C36950
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-569 <MAE>
 A;Cross-references: UNIPROT:Q07397; GB:D14439; NID:9393296; PIDN:BAA03325_1; PID:9216362
 C;Superfamily: Uracil, alpha subunit; uracil 62K chain homology
 C;Keywords: hydrolase

F,5-552/Domain: urease 62K chain homology <U62>

Query Match 84.8%; Score 28; DB 2; Length 569;
Best Local Similarity 57.1%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0;
Gaps 0;

Qy 2 PXRPEKLL 8
| ||| :
Db 302 PTRPYTI 308

Search completed: March 28, 2005, 08:38:06
Job time : 42 secs

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GenCore version 5.1.6
(Without alignments)

57.583 Million cell updates/sec

Om protein - protein search, using sw model

Run on:

March 28, 2005, 08:33:43 ; Search time 46 Seconds

(without alignments)

US-10-036-918B-4

Perfect score: 33

Sequence: 1 XPXRRPYXL 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 200000000

post-processing: Minimum Match 0%

Listing first 100 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/us07_pubcomb.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCTN_NEW_PUB_pep:*

3: /cgn2_6/ptodata/2/pubpaa/us06_pubcomb.pep:*

4: /cgn2_6/ptodata/2/pubpaa/us06_pubcomb.pep:*

5: /cgn2_6/ptodata/2/pubpaa/us07_NEW_PUB_pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTRS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/us07_pubcomb.pep:*

8: /cgn2_6/ptodata/2/pubpaa/us08_PUBCOMB_pep:*

9: /cgn2_6/ptodata/2/pubpaa/us09_pubcomb.pep:*

10: /cgn2_6/ptodata/2/pubpaa/us09C_PUBCOMB_pep:*

11: /cgn2_6/ptodata/2/pubpaa/us10_PUBCOMB_pep:*

12: /cgn2_6/ptodata/2/pubpaa/us09_NEW_PUB_pep:*

13: /cgn2_6/ptodata/2/pubpaa/us10A_PUBCOMB_pep:*

14: /cgn2_6/ptodata/2/pubpaa/us10B_PUBCOMB_pep:*

15: /cgn2_6/ptodata/2/pubpaa/us10C_PUBCOMB_pep:*

16: /cgn2_6/ptodata/2/pubpaa/us10D_PUBCOMB_pep:*

17: /cgn2_6/ptodata/2/pubpaa/us10_NEW_PUB_pep:*

18: /cgn2_6/ptodata/2/pubpaa/us11_NEW_PUB_pep:*

19: /cgn2_6/ptodata/2/pubpaa/us60_NEW_PUB_pep:*

20: /cgn2_6/ptodata/2/pubpaa/us60_PUBCOMB_pep:*

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	29	87.9	65	16 US-10-437-963-11056
2	29	87.9	78	15 US-10-424-599-232159
3	29	87.9	129	15 US-10-599-257546
4	29	87.9	157	15 US-10-094-749-2431
5	29	87.9	216	9 US-00-863-200-4
6	29	87.9	247	15 US-10-407-079-106
7	29	87.9	281	15 US-10-283-122A-72786
8	29	87.9	312	15 US-10-283-122A-54324
9	29	87.9	315	9 US-00-815-242-11014
10	29	87.9	315	15 US-10-283-122A-58158
11	29	87.9	315	15 US-10-283-122A-67564
12	29	87.9	316	9 US-00-815-242-11934
13	29	87.9		

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

score . No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
US-10-437-963-110356 Application US/10437963
; Sequence 110356, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbakuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 110356.
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT4530_14427C.1.pep
; US-10-437-963-110356

Query Match 87.9%; Score 29; DB 15; Length 65;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 2
US-10-424-599-232759 Application US/10424599
; Sequence 232759, Application US/10424599
; Publication No. US2004031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbakuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424-599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 257546
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_74589C.1.pep
; US-10-424-599-232759

Query Match 87.9%; Score 29; DB 15; Length 129;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 3
US-10-424-599-232759 Application US/10424599
; Sequence 257546, Application US/10424599
; Publication No. US2004031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbakuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424-599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 257546
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_74589C.1.pep
; US-10-424-599-232759

Query Match 87.9%; Score 29; DB 15; Length 129;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 4
US-10-094-749-2431 Application US/10094749
; Sequence 2431, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISOMO, YUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RIYOTARO
; APPLICANT: TANECHITA, ICHIRO
; APPLICANT: SEKI, NAOKI
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKI
; APPLICANT: NAGARI, KENJI
; APPLICANT: MASUHO, YASUHIKO

TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
PRIORITY FILING DATE: 2002-03-12
PRIORITY APPLICATION NUMBER: 60/350,435
PRIORITY FILING DATE: 2002-01-24
PRIORITY APPLICATION NUMBER: JP 2001-328381
PRIORITY FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 2431
LENGTH: 157
TYPE: PRT
ORGANISM: Homo sapiens
;US-10-094-749-2431
Query Match Score 29; DB 15; Length 157;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPyXL 8
Db 43 PNRPYTL 49
RESULT 5
US-09-863-200-4
Sequence 4, Application US/09863200
Publication No. US20020039762A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc
TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 38155-20014.00
CURRENT APPLICATION NUMBER: US/09/863, 200
CURRENT FILING DATE: 2001-05-22
PRIORITY APPLICATION NUMBER: US 60/206, 019
PRIOR FILING DATE: 2000-05-22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 4
LENGTH: 216
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus amino acid
US-09-863-200-4
Query Match Score 29; DB 9; Length 216;
Best Local Similarity 71.4%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPyXL 8
Db 191 PDRPySL 197
RESULT 6
US-10-407-079-106
Sequence 4, Application US/09863200
Publication No. US20020039762A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Glucksmann, Maria A.
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Carroll, Joseph M.
APPLICANT: Galvin, Katherine M.
TITLE OF INVENTION: 1836, 2466, 43238, 1983, 52881, 2398, AND 26908 MOLECULES AND USES THEREFOR
FILE REFERENCE: MP103-0510NM
CURRENT APPLICATION NUMBER: US/10/407, 079
CURRENT FILING DATE: 2003-04-03
TYPE: PRT
ORGANISM: Homo sapiens
;US-10-094-749-2431
Query Match Score 29; DB 15; Length 157;
Best Local Similarity 71.4%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPyXL 8
Db 191 PDRPySL 197
RESULT 7
US-10-424-599-201130
Sequence 4, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21-(53223)
CURRENT APPLICATION NUMBER: US/10/424, 599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO: 201130
LENGTH: 247
TYPE: PRT
ORGANISM: Glycine max
;US-10-424-599-201130
Query Match Score 29; DB 15; Length 247;
Best Local Similarity 71.4%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPyXL 8
Db 191 PDRPySL 197
RESULT 8
US-10-407-079-106
Sequence 4, Application US/09863200
Publication No. US20020039762A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Glucksmann, Maria A.
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Carroll, Joseph M.
APPLICANT: Galvin, Katherine M.
TITLE OF INVENTION: 1836, 2466, 43238, 1983, 52881, 2398, AND 26908 MOLECULES AND USES THEREFOR
FILE REFERENCE: MP103-0510NM
CURRENT APPLICATION NUMBER: US/10/407, 079
CURRENT FILING DATE: 2003-04-03
TYPE: PRT
ORGANISM: Glycine max
;US-10-407-079-106
Query Match Score 29; DB 15; Length 157;
Best Local Similarity 71.4%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPyXL 8
Db 191 PDRPySL 197
RESULT 9
US-10-424-599-201130
Sequence 4, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21-(53223)
CURRENT APPLICATION NUMBER: US/10/424, 599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO: 201130
LENGTH: 247
TYPE: PRT
ORGANISM: Glycine max
;US-10-424-599-201130
Query Match Score 29; DB 15; Length 247;
Best Local Similarity 71.4%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 80 PARBYFL 86 Publication No. US20040029129A1

RESULT 8 GENERAL INFORMATION:

; Sequence 72786, Application US/10282122A
; Publication No. US20040029129A1 APPLICANT: Wang, Liangsu

; GENERAL INFORMATION: APPLICANT: Zamudio, Carlos

; APPLICANT: Wang, Liangsu APPLICANT: Malone, Cheryl

; APPLICANT: Zamudio, Carlos APPLICANT: Haselbeck, Robert

; APPLICANT: Malone, Cheryl APPLICANT: Olsen, Kari

; APPLICANT: Haselbeck, Robert APPLICANT: Zyskind, Judith

; APPLICANT: Olsen, Kari APPLICANT: Wall, Daniel

; APPLICANT: Zyskind, Judith APPLICANT: Trawick, John

; APPLICANT: Carr, Grant APPLICANT: Yamamoto, Robert

; APPLICANT: Carr, Grant APPLICANT: Forsyth, R.

; APPLICANT: Yamamoto, Robert APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA-034A FILE REFERENCE: ELITRA-034A

; CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20 CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078 PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21 PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848 PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23 PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727 PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335 PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06 PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,,347 PRIOR APPLICATION NUMBER: 60/230,,347

; PRIOR FILING DATE: 2000-09-09 PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578 PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23 PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625 PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27 PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,,931 PRIOR APPLICATION NUMBER: 60/257,,931

; PRIOR FILING DATE: 2000-12-22 PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636 PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308 PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16 PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM. Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614 NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: Patentin version 3.1 SOFTWARE: Patentin version 3.1

; SEQ ID NO 72786 SEQ ID NO 54324

; LENGTH: 281 LENGTH: 312

; TYPE: PRT TYPE: PRT

; ORGANISM: Salmonella paratyphi A ORGANISM: Campylobacter jejuni

; FEATURE: MISC FEATURE

; NAME/KEY: MISC FEATURE

; LOCATION: (103).-(103)

; OTHER INFORMATION: X=any amino acid

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (256)..(256)

; OTHER INFORMATION: X=any amino acid

US-10-282-122A-72786 Query Match 87.9%; Score 29; DB 15; Length 281; Best Local Similarity 71.4%; Pred. No. 5.7e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8 Db 60 PDPRYAL 66

RESULT 10 Query Match 87.9%; Score 29; DB 15; Length 312; Best Local Similarity 71.4%; Pred. No. 6.3e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

US-09-815-242-11014 Sequence 11014, Application US/09815242

; General Information: Patent No. US2002001569A1

; General Information: APPLICANT: Haselbeck, Robert

; APPLICANT: Haselbeck, Robert APPLICANT: Olsen, Kari L.

; APPLICANT: Olsen, Kari L. APPLICANT: Zyskind, Judith W.

; APPLICANT: Zyskind, Judith W. APPLICANT: Wall, Daniel

; APPLICANT: Wall, Daniel APPLICANT: Carr, John D.

; APPLICANT: Carr, John D. APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in Title of Invention: Prokaryotes

; FILE REFERENCE: ELITRA-011A CURRENT APPLICATION NUMBER: US/09/815,242

RESULT 9 Sequence 54324, Application US/10282122A

US-10-282-122A-54324

CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 1-1110
 SOFTWARE: FaberSEQ for Windows Version 4.0
 SEQ ID NO: 11014

LENGTH: 315
 TYPE: PRT
 ORGANISM: Haemophilus influenzae
 US-09-815-242-11014

Query Match 87.9%; Score 29; DB 9; Length 315;
 Best Local Similarity 71.4%; Pred. No. 6.3e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 66 PNRPyTL 72

RESULT 11
 US-10-282-122A-58158
 ; Sequence 58158, Application US/10282122A
 ; Publication No. US20040029129A1

GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert

APPLICANT: Olszen, Kari
 APPLICANT: Zykkind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.

APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA 034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-03-20

PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-05
 PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 76114
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 67564

LENGTH: 315
 TYPE: PRT
 ORGANISM: Pseudomonas putida
 US-10-282-122A-67564

Query Match 87.9%; Score 29; DB 15; Length 315;
 Best Local Similarity 71.4%; Pred. No. 6.3e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 66 PNRPyTL 72

RESULT 12
 US-10-282-122A-67564
 ; Sequence 67564, Application US/10282122A
 ; Publication No. US20040029129A1

GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert

APPLICANT: Olszen, Kari
 APPLICANT: Zykkind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.

APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA 034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-03-20

PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-05
 PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16

Db | ||| |
 67 PKRPyTL 73

RESULT 13
 Sequence 11934, Application US/09815242
 Patent No. US2002061569A1
 GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes
 FILE REFERENCE: ELITRA.011A
 CURRENT APPLICATION NUMBER: US/09/815, 242
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191, 078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206, 848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/230, 335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230, 347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242, 572
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253, 625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257, 931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267, 636
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267, 636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269, 308
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 11934
 LENGTH: 316
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11934

Query Match Score 29; DB 9; Length 316;
 Best Local Similarity 71.4%; Pred. No. 6.3e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 67 PKRPyTL 73

RESULT 14
 US-10-282-122A-66513
 Sequence 66513, Application US/10282122A
 Publication No. US20040029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zanudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282, 122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191, 078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206, 848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207, 727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230, 335
 PRIOR FILING DATE: 2000-09-05
 PRIOR APPLICATION NUMBER: 60/230, 347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242, 578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253, 625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257, 931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267, 636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269, 308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 66513
 LENGTH: 316
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66513

Query Match Score 29; DB 15; Length 316;
 Best Local Similarity 71.4%; Pred. No. 6.3e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 67 PKRPyTL 73

RESULT 15
 US-10-282-122A-66958
 Sequence 66958, Application US/10282122A
 Publication No. US20040029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zanudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282, 122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191, 078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206, 848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207, 727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230, 335
 PRIOR FILING DATE: 2000-09-05
 PRIOR APPLICATION NUMBER: 60/230, 347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242, 578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253, 625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257, 931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267, 636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269, 308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.

PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66958
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Pasteurella multocida
; US-10-282-122A-66958

Query Match 87.9%; Score 29; DB 15; Length 317;
; Best Local Similarity 71.4%; Pred. No. 6.4e+02; Indels 0; Gaps 0;
; Matches 5; Conservative 0; Mismatches 2;

Qy	2 PXRPyXL 8
Db	69 PRPPyTL 75

RESULT 16
US-10-282-122A-70135
; Sequence 70135, Application US/10282122A
; Publication No. US20040209129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangfu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haebeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA_011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10048
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-815-242-10048

Query Match 87.9%; Score 29; DB 9; Length 319;
; Best Local Similarity 71.4%; Pred. No. 6.4e+02; Indels 0; Gaps 0;
; Matches 5; Conservative 0; Mismatches 2;

Qy	2 PXRPyXL 8
Db	70 PQRPYTL 76

RESULT 18
US-09-815-242-13897
; Sequence 13897, Application US/09815242
; Patent No. US20020051569A1
; GENERAL INFORMATION:
; APPLICANT: Haebeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes

FILE REFERENCE: ELITRA_011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/1207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO: 13897

LENGTH: 319

TYPE: PRT

ORGANISM: Salmonella typhi

US-09-815-242-13897

Query Match 87.9%; Score 29; DB 9; Length 319; Best Local Similarity 71.4%; Pred. No. 6.4e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DY 2 PYRPyXL 8
Dy 70 PORPyXL 76

RESULT 19

US-10-282-122A-43192

Sequence 43192, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA_034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 43192

LENGTH: 319

TYPE: PRT

ORGANISM: Escherichia coli

US-10-282-122A-43192

Query Match 87.9%; Score 29; DB 15; Length 319; Best Local Similarity 71.4%; Pred. No. 6.4e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DY 2 PYRPyXL 8
Dy 70 PORPyXL 76

RESULT 20

US-10-282-122A-55833

Sequence 55833, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA_034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 55833

LENGTH: 319

TYPE: PRT

ORGANISM: Enterobacter cloacae

US-10-282-122A-55833

Query Match 87.9%; Score 29; DB 15; Length 319;

Best Local Similarity 71.4%; Pred. No. 6.4e+02; Mismatches 2; Indels 0; Gaps 0;

RESULT 21
US-10-282-122A-59606
; Sequence 59606, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EULTRA.034A
; CURRENT APPLICATION NUMBER: US/10/282, 122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191, 078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206, 848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207, 727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230, 335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230, 347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/207, 727
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253, 625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257, 931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267, 636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269, 308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 59606
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-10-282-122A-65080
; Query Match 87.9%; Score 29; DB 15; Length 319;
; Best Local Similarity 71.4%; Pred. No. 6.4e+02; Mismatches 2; Indels 0; Gaps 0;
; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
; QY 2 PXRPyXL 8
; DB 70 PRRPyTL 76
; RESULT 23
US-10-282-122A-65894
; Sequence 65894, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EULTRA.034A
; CURRENT APPLICATION NUMBER: US/10/282, 122A
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EULTRA.034A
; CURRENT APPLICATION NUMBER: US/10/282, 122A
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

RESULT 22
US-10-282-122A-65080
; Sequence 65080, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu

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; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68594
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-282-122A-68594

Query Match 87.9%; Score 29; DB 15; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PRPYXL 8
Db 67 PRPYYL 73
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-10-282-122A-68569

Query Match 87.9%; Score 29; DB 15; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PRXPYXL 8
Db 70 PRPYYL 76
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Application US/10282122A
US-10-282-122A-75293

; Sequence 75293, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA_034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75293
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Salmonella typhimurium

```

US-10-282-122A-75293

Publication No. US20040029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Ohlen, Kari
 APPLICANT: Haselbeck, Robert
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.

Query Match 87.9%; Score 29; DB 15; Length 319;
 Best Local Similarity 71.4%; Pred. No. 6.4e+02; 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
 Db 70 PQRPYTL 76

RESULT 26

US-10-282-122A-76171
 Sequence 76171, Application US/10282122A
 Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Ohlen, Kari
 APPLICANT: Haselbeck, Robert
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIORITY APPLICATION NUMBER: 60/191,078

PRIORITY FILING DATE: 2000-03-21

PRIORITY APPLICATION NUMBER: 60/206,848

PRIORITY FILING DATE: 2000-05-23

PRIORITY APPLICATION NUMBER: 60/207,727

PRIORITY FILING DATE: 2000-05-26

PRIORITY APPLICATION NUMBER: 60/191,078

PRIORITY FILING DATE: 2000-03-21

PRIORITY APPLICATION NUMBER: 60/206,848

PRIORITY FILING DATE: 2000-05-23

PRIORITY APPLICATION NUMBER: 60/230,347

PRIORITY FILING DATE: 2000-09-09

PRIORITY APPLICATION NUMBER: 60/230,347

PRIORITY FILING DATE: 2000-10-23

PRIORITY APPLICATION NUMBER: 60/242,578

PRIORITY FILING DATE: 2000-11-27

PRIORITY APPLICATION NUMBER: 60/253,625

PRIORITY FILING DATE: 2000-12-22

PRIORITY APPLICATION NUMBER: 60/267,636

PRIORITY FILING DATE: 2001-02-09

PRIORITY APPLICATION NUMBER: 60/242,578

PRIORITY FILING DATE: 2000-10-23

PRIORITY APPLICATION NUMBER: 60/253,625

PRIORITY FILING DATE: 2000-11-27

PRIORITY APPLICATION NUMBER: 60/267,636

PRIORITY FILING DATE: 2001-02-16

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-12-22

PRIORITY APPLICATION NUMBER: 60/269,308

PRIORITY FILING DATE: 2001-02-09

PRIORITY APPLICATION NUMBER: 60/269,308

PRIORITY FILING DATE: 2000-11-27

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-12-22

PRIORITY APPLICATION NUMBER: 60/269,308

PRIORITY FILING DATE: 2001-02-16

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-11-27

PRIORITY APPLICATION NUMBER: 60/269,308

PRIORITY FILING DATE: 2001-02-16

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-11-27

PRIORITY APPLICATION NUMBER: 60/269,308

PRIORITY FILING DATE: 2001-02-16

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-11-27

PRIORITY APPLICATION NUMBER: 60/269,308

PRIORITY FILING DATE: 2001-02-16

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-11-27

PRIORITY APPLICATION NUMBER: 60/269,308

PRIORITY FILING DATE: 2001-02-16

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-11-27

PRIORITY APPLICATION NUMBER: 60/269,308

PRIORITY FILING DATE: 2001-02-16

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-11-27

PRIORITY APPLICATION NUMBER: 60/269,308

PRIORITY FILING DATE: 2001-02-16

PRIORITY APPLICATION NUMBER: 60/257,931

PRIORITY FILING DATE: 2000-11-27

SEQUENCE ID NO: 76171

LENGTH: 319

TYPE: PRT

ORGANISM: Salmonella typhi

US-10-282-122A-76171

Query Match 87.9%; Score 29; DB 15; Length 319;

Best Local Similarity 71.4%; Pred. No. 6.4e+02; 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
 Db 70 PQRPYTL 76

RESULT 27

US-10-282-122A-77412

Sequence 77412, Application US/10282122A

; Sequence 77412, Application US/10282122A

; Sequence 77412, Application US/10282122A

RESULT 27

US-10-282-122A-77412

; Sequence 77412, Application US/10282122A

FILE REFERENCE: ELITRA.034A
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 CURRENT APPLICATION NUMBER: US/10/282,122A
 PRIOR FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-09-10
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 77971
 LENGTH: 319
 TYPE: PRT
 ORGANISM: Yersinia pestis
 S-10-282-122A-77971
 Query Match 87.9%; Score 29; DB 15; Length 319;
 Best Local Similarity 71.4%; Pred. No. 6.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PRXPYX 8
 Db 71 PRXPYTL 77
 RESULT 29
 Sequence 68469, Application US/10282122A
 Publication No. US20040029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlben, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forbyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 51090
 LENGTH: 320
 TYPE: PRT
 ORGANISM: Proteus mirabilis
 US-10-282-122A-68469
 Query Match 87.9%; Score 29; DB 15; Length 320;
 Best Local Similarity 71.4%; Pred. No. 6.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PRXPYX 8
 Db 71 PRXPYTL 77
 RESULT 30
 Sequence 51090, Application US/10282122A
 Publication No. US20040029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlben, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forbyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 51090

```

; LENGTH: 321
; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-10-282-122A-51090

Query Match      Best Local Similarity 87.9%; Score 29; DB 15; Length 321;
Matches         5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy          2 PXRPYXL 8
Db          67 PQRPYTL 73

RESULT 31
US-10-282-122A-47697
Sequence 47697, Application US/10282122A
Publication No. US20040029129A1

GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohisen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forryth, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 50581
LENGTH: 323
TYPE: PRT
ORGANISM: Burkholderia mallei
US-10-282-122A-50581

Query Match      Best Local Similarity 87.9%; Score 29; DB 15; Length 323;
Matches         5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy          2 PXRPYXL 8
Db          67 PQRPYTL 73

RESULT 33
US-10-424-599-215226
Sequence 215226, Application US/10424599
Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou Yiliua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28

Query Match      Best Local Similarity 87.9%; Score 29; DB 15; Length 323;
Matches         5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy          2 PXRPYXL 8
Db          67 PQRPYTL 73

```

NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 215226
LENGTH: 331
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_36374C.1.pep
US-10-424-599-215226

Query Match 87.9%; Score 29; DB 15; Length 331;
Best Local Similarity 71.4%; Pred. No. 6.6e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPYXXL 8
Db 293 PSRPyYL 299

RESULT 34
US-10-437-963-145135
Sequence 145135, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 145135
LENGTH: 392
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_45883C.1.pep
US-10-437-963-145135

Query Match 87.9%; Score 29; DB 16; Length 392;
Best Local Similarity 71.4%; Pred. No. 7.8e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPYXXL 8
Db 364 PTBPyQL 370

RESULT 35
US-10-278-141-4
Sequence 4, Application US/10278141
; Publication No. US20030138818A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: LU, Duying Aina M.
; APPLICANT: THORNTON, Michael
; APPLICANT: LU, Yan
; APPLICANT: TRIBOURY, Catherine M.
; APPLICANT: GRAUL, Richard
; APPLICANT: KHAN, Farrah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: NGUYEN, Damniel B.
; APPLICANT: LIU, Yan
; APPLICANT: HAFALIA, Catherine M.
; APPLICANT: GRAUL, Richard
; APPLICANT: LUO, Duying Aina M.
; APPLICANT: THORNTON, Michael
; APPLICANT: VUE, Henry
; APPLICANT: HAFALIA, Catherine M.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: LAL, Preeti
; APPLICANT: REDDY, Roopa
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: TANG, Y. Tom
; APPLICANT: AU-YOUNG, Janice
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0096_PCT
CURRENT APPLICATION NUMBER: US/10/296,081
PRIORITY FILING DATE: 2002-11-18
PRIORITY APPLICATION NUMBER: 60/205,628, 60/205,222, 60/207,566; 60/208,834; 60/208,861
PRIORITY FILING DATE: 2000-05-18; 2000-05-22; 2000-05-25; 2000-06-02; 2000-06-02
SOFTWARE: PERL Program
SEQ ID NO 4
LENGTH: 432
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030138818A1 1258785CD1
US-10-278-141-4

Query Match 87.9%; Score 29; DB 14; Length 432;
Best Local Similarity 71.4%; Pred. No. 8.6e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPYXXL 8
Db 393 PDPrYSL 399

RESULT 36
US-10-296-091-4
Sequence 4, Application US/10296081
; Publication No. US20030220477A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: LU, Duying Aina M.
; APPLICANT: THORNTON, Michael
; APPLICANT: LU, Yan
; APPLICANT: TRIBOURY, Catherine M.
; APPLICANT: GRAUL, Richard
; APPLICANT: KHAN, Farrah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: NGUYEN, Damniel B.
; APPLICANT: LIU, Yan
; APPLICANT: HAFALIA, Catherine M.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: LAL, Preeti
; APPLICANT: REDDY, Roopa
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: TANG, Y. Tom
; APPLICANT: AU-YOUNG, Janice
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0096_PCT
CURRENT APPLICATION NUMBER: US/10/296,081
PRIORITY FILING DATE: 2002-11-18
PRIORITY APPLICATION NUMBER: 60/205,628, 60/205,222, 60/207,566; 60/208,834; 60/208,861
PRIORITY FILING DATE: 2000-05-18; 2000-05-22; 2000-05-25; 2000-06-02; 2000-06-02
SOFTWARE: PERL Program
SEQ ID NO 4

LENGTH: 432
TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: misc feature

NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030220477A1 1258785CD1

US-10-296-081-4

Qy	2	PXRPyXL 8	Db	393	PDRPySL 399

RESULT 37
US-10-400-991-20
; Sequence 20, Application US/104000991
; Publication No. US20030224417A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Weich, Nadine S.
; APPLICANT: Hunter, John J.
; APPLICANT: White, David
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Chun, Myoung
TITLE OF INVENTION: 14400, 2838, 14618, 15334, 14274, 32164,
TITLE OF INVENTION: 39404, 38911, 26904, 31237, 18057, 16405,
TITLE OF INVENTION: 27423, 32700, 32712 AND 12216, NOVEL SEVEN TRANSMEMBRANE
TITLE OF INVENTION: PROTEIN-PROTEIN COUPLES RECEPTORS

CURRENT APPLICATION NUMBER: US/10/400,991
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13950

LENGTH: 455
TYPE: PRT

ORGANISM: Streptomyces avermitilis
US-10-156-761-13950

Query Match 87.9%; Score 29; DB 15; Length 432;
Best Local Similarity 71.4%; Pred. No. 8.6e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Indels 0; Gaps 0;

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 83
SOFTWARE: PastelSQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 450
TYPE: PRT

ORGANISM: Homo Sapiens
US-10-400-991-20

Query Match 87.9%; Score 29; DB 15; Length 450;
Best Local Similarity 71.4%; Pred. No. 8.9e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Indels 0; Gaps 0;

Indels 0; Gaps 0;

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 83
SOFTWARE: PastelSQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 450
TYPE: PRT

ORGANISM: Homo Sapiens
US-10-400-991-20

Query Match 87.9%; Score 29; DB 15; Length 569;
Best Local Similarity 71.4%; Pred. No. 1.1e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Indels 0; Gaps 0;

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 83
SOFTWARE: PastelSQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 450
TYPE: PRT

ORGANISM: Homo Sapiens
US-10-400-991-20

Query Match 87.9%; Score 29; DB 15; Length 450;
Best Local Similarity 71.4%; Pred. No. 8.9e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Indels 0; Gaps 0;

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 83
SOFTWARE: PastelSQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 450
TYPE: PRT

ORGANISM: Homo Sapiens
US-10-400-991-20

Db 411 PDRPySL 417
RESULT 38
US-10-156-761-13950
; Sequence 13950, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAO
; APPLICANT: SAKAKI, YOSHIO
; APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13950

LENGTH: 455
TYPE: PRT

ORGANISM: Streptomyces avermitilis
US-10-156-761-13950

Query Match 87.9%; Score 29; DB 14; Length 455;
Best Local Similarity 71.4%; Pred. No. 9e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Indels 0; Gaps 0;

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 83
SOFTWARE: PastelSQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 450
TYPE: PRT

ORGANISM: Homo Sapiens
US-10-400-991-20

Query Match 87.9%; Score 29; DB 15; Length 569;
Best Local Similarity 71.4%; Pred. No. 1.1e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Indels 0; Gaps 0;

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 83
SOFTWARE: PastelSQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 450
TYPE: PRT

ORGANISM: Homo Sapiens
US-10-400-991-20

Query Match 87.9%; Score 29; DB 15; Length 569;
Best Local Similarity 71.4%; Pred. No. 1.1e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Indels 0; Gaps 0;

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 83
SOFTWARE: PastelSQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 450
TYPE: PRT

ORGANISM: Homo Sapiens
US-10-400-991-20

Query Match 87.9%; Score 29; DB 15; Length 569;
Best Local Similarity 71.4%; Pred. No. 1.1e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Indels 0; Gaps 0;

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 83
SOFTWARE: PastelSQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 450
TYPE: PRT

ORGANISM: Homo Sapiens
US-10-400-991-20

Query Match 87.9%; Score 29; DB 15; Length 569;
Best Local Similarity 71.4%; Pred. No. 1.1e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Indels 0; Gaps 0;

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 83
SOFTWARE: PastelSQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 450
TYPE: PRT

ORGANISM: Homo Sapiens
US-10-400-991-20

Query Match 87.9%; Score 29; DB 15; Length 569;
Best Local Similarity 71.4%; Pred. No. 1.1e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Indels 0; Gaps 0;

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 83
SOFTWARE: PastelSQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 450
TYPE: PRT

ORGANISM: Homo Sapiens
US-10-400-991-20

Query Match 87.9%; Score 29; DB 15; Length 569;
Best Local Similarity 71.4%; Pred. No. 1.1e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Indels 0; Gaps 0;

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 83
SOFTWARE: PastelSQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 450
TYPE: PRT

ORGANISM: Homo Sapiens
US-10-400-991-20

RESULT 40
US-10-425-114-51274
; Sequence 51274, Application US/10425114
; Publication No. US2004003488A1
GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 51274
LENGTH: 747
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3150-094-A6_FLI.pep

US-10-425-114-51274

Query Match 87.9%; Score 29; DB 15; Length 747;
Best Local Similarity 71.4%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PKAPYXL 8
Db 154 PSRPyLL 160

search completed: March 28, 2005, 08:39:57
Job time : 47 secs

OM protein - protein search, using sw model									
Run on:	Copyright (c) 1993 - 2005 Compugen Ltd.								
GenCore version 5.1.6									
Title:	US-10-036-918B-4	29	28	84.8	12	3	US-09-202-832A-4	29	28
Perfect score:	33	30	28	84.8	13	1	US-07-714-540-8	30	28
Sequence:	1 XPKRPYKL 8	31	28	84.8	13	2	US-08-747-137-17	31	28
Scoring table:	BLOSUM62	32	28	84.8	13	2	US-08-737-299A-1	32	28
	Gapext 10.0 , Gapext 0.5	33	28	84.8	13	3	US-09-334-254A-1	33	28
Searched:	51345 seqs, 1464964 residues	34	28	84.8	13	3	US-09-289-693-1	34	28
Total number of hits satisfying chosen parameters:	513545	35	28	84.8	13	3	US-09-355-869-2	35	28
Minimum DB seq length:	0	36	28	84.8	13	3	US-09-605-991-8	36	28
Maximum DB seq length:	200000000	37	28	84.8	13	4	US-09-420-797B-8	37	28
Post-processing:	Minimum Match 0%	38	28	84.8	13	4	US-09-609-534-8	38	28
	Maximum Match 100%	39	28	84.8	13	4	US-09-528-200-10	39	28
	Listing first 100 summaries	40	28	84.8	13	4	US-09-528-200-161	40	28
Database :	Issued Patents AA: *	41	28	84.8	13	4	US-09-528-200-162	41	28
	1: /cgn2_6/prodata/1/iaa/5A_COMB_pep: *	42	28	84.8	13	4	US-09-528-200-163	42	28
	2: /cgn2_6/prodata/1/iaa/5B_COMB_pep: *	43	28	84.8	13	4	US-09-528-200-164	43	28
	3: /cgn2_6/prodata/1/iaa/6A_COMB_pep: *	44	28	84.8	13	4	US-10-265-099-1	44	28
	4: /cgn2_6/prodata/1/iaa/6B_COMB_pep: *	45	28	84.8	13	4	US-10-272-272-4	45	28
	5: /cgn2_6/prodata/1/iaa/PCTUS_COMBO_pep: *	46	28	84.8	134	5	PCT-US93-07213-15	46	28
	6: /cgn2_6/prodata/1/iaa/backfile1.pep: *	47	28	84.8	165	4	US-09-489-039A-137	47	28
	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	48	28	84.8	169	3	US-09-002-114-3	48	28
		49	28	84.8	169	3	US-09-002-114-4	49	28
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		51	28	84.8	171	4	US-09-949-016-7377	51	28
		52	28	84.8	186	4	US-09-248-796A-160	52	28
		53	28	84.8	231	4	US-09-902-540-1080	53	28
		54	28	84.8	240	4	US-09-902-540-1600	54	28
		55	28	84.8	281	4	US-09-248-796A-166	55	28
		56	28	84.8	317	4	US-09-252-991A-293	56	28
		57	28	84.8	322	4	US-09-902-540-1523	57	28
		58	28	84.8	567	4	US-09-328-352-5912	58	28
		59	28	84.8	568	1	US-07-732-242C-3	59	28
		60	28	84.8	1279	4	US-09-170-496-A-293	60	28
		61	28	84.8	1279	4	US-09-364-425B-58	61	28
		62	27	81.8	169	4	US-09-270-767-3783	62	27
		63	27	81.8	169	4	US-09-767-5304	63	27
		64	27	81.8	551	4	US-09-489-039A-951	64	27
		65	27	81.8	526	3	US-09-129-075-4	65	27
		66	27	81.8	726	3	US-09-346-237-3	66	27
		67	27	81.8	726	3	US-09-346-237-13	67	27
		68	27	81.8	726	4	US-09-544-123-4	68	27
		69	27	81.8	915	3	US-09-544-237-2	69	27
		70	26	78.8	20	3	US-08-602-999A-314	70	26
		71	26	78.8	20	4	US-09-500-124-314	71	26
		72	26	78.8	46	3	US-09-640-737-43	72	26
		73	26	78.8	100	4	US-09-252-991A-320	73	26
		74	26	78.8	105	1	US-09-482-577B-27	74	26
		75	26	78.8	105	3	US-09-482-577B-27	75	26
		76	26	78.8	105	3	US-09-289-222B-31	76	26
		77	26	78.8	105	3	US-09-218-176-10	77	26
		78	26	78.8	105	3	US-09-054-526B-31	78	26
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		83	26	78.8	105	4	US-09-220-616-169	83	26
		84	26	78.8	105	4	US-09-374-95C-61	84	26
		85	26	78.8	105	4	US-09-220-617-169	85	26
		86	26	78.8	105	4	US-09-220-407-169	86	26
		87	26	78.8	105	4	US-09-378-235-36	87	26
		88	26	78.8	106	4	US-09-248-796A-156	88	26
		89	26	78.8	107	4	US-09-541-681A-826	89	26
		90	26	78.8	121	1	US-09-481-377-1	90	26
		91	26	78.8	121	2	US-09-491-835-18	91	26
		92	26	78.8	121	3	US-09-151-733A-20	92	26
		93	26	78.8	121	3	US-09-96-092A-18	93	26
		94	26	78.8	121	3	US-09-172-062-18	94	26
		95	26	78.8	121	3	US-09-301-520D-18	95	26
		96	26	78.8	121	3	US-09-389-705-20	96	26
		97	26	78.8	121	5	PCT-US94-00666-20	97	26
		98	26	78.8	121	5	PCT-US94-00685-18	98	26
		99	26	78.8	122	1	US-08-581-529B-16	99	26
		100	26	78.8	122	1	US-08-455-559-22	100	26

ALIGNMENTS

RESULT 1
US-08-357-598-11
; Sequence 11, Application US/08357598
; Patent No. 5,705,625
; GENERAL INFORMATION:
; APPLICANT: Civin, Curt I.
; APPLICANT: Small, Donald
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK3
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,598
; FILING DATE: 15-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/033001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5099
; TELEFAX: 619/678-5099
; LENGTH: 1100 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. 5916792 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-357-598-11

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1100 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-357-598-11

Query Match 90.9%; Score 30; DB 1; Length 1100;
Best Local Similarity 71.4%; Pred. No. 4.3e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY | | | |
Db 228 PSRPYAL 234

RESULT 3
PCT-US95-16435-11
; Sequence 11, Application PC/TUS9516435
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK3
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16435
; FILING DATE: 15-DEC-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/033001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; LENGTH: 1100 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-16435-11

Query Match 90.9%; Score 30; DB 5; Length 1100;
 Best Local Similarity 71.4%; Pred. No. 4,3e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 228 PSRPyAL 234

RESULT 4
 Sequence 6625, Application US/09543681A
 Patent No. 6605709

GENERAL INFORMATION:
 APPLICANT: GARY BRETON
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709.1002-001
 CURRENT APPLICATION NUMBER: US/09/543,681A
 PRIOR APPLICATION NUMBER: US 60/128,706
 PRIOR FILING DATE: 1999-04-09
 NUMBER OF SEQ ID NOS: 8344
 SEQ ID NO 6625
 LENGTH: 323
 TYPE: PRT
 ORGANISM: Proteus mirabilis
 US-09-543-681A-6625

Query Match 87.9%; Score 29; DB 4; Length 323;
 Best Local Similarity 71.4%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 74 PLRPyTL 80

RESULT 5
 Sequence 12281, Application US/09489039A
 Patent No. 6610836

GENERAL INFORMATION:
 APPLICANT: GARY BRETON et. al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709.200401
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 12281
 LENGTH: 323
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-12281

RESULT 5
 Sequence 12281, Application US/09489039A
 Patent No. 6610836

GENERAL INFORMATION:
 APPLICANT: GARY BRETON et. al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709.200401
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 12281
 LENGTH: 323
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-12281

Query Match 87.9%; Score 29; DB 4; Length 323;
 Best Local Similarity 71.4%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 74 PLRPyTL 80

RESULT 5
 Sequence 12281, Application US/09489039A
 Patent No. 6610836

GENERAL INFORMATION:
 APPLICANT: GARY BRETON et. al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709.200401
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 12281
 LENGTH: 323
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-12281

Query Match 87.9%; Score 29; DB 4; Length 323;
 Best Local Similarity 71.4%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 74 PLRPyTL 80

RESULT 6
 Sequence 4495, Application US/09543681A
 Patent No. 6605709

GENERAL INFORMATION:

RESULT 6
 Sequence 4495, Application US/09543681A
 Patent No. 6605709

GENERAL INFORMATION:
 APPLICANT: Ihle, James N.
 APPLICANT: Silvernoinen, Ollie
 APPLICANT: Wittluhn, Bruce A.
 APPLICANT: Quelle, Frederick W.
 TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine Signal
 TITLE OF INVENTION: Transduction
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Steiner, Kessler, Goldstein & Fox
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.

; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNITS, CARTSEN
; APPLICANT: VOLLMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGNER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; TITLE OF INVENTION: FOR OPTICAL DIAGNOSIS
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; CURRENT FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713 9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 179
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; OTHER INFORMATION: US-09-528-200-179

Query Match
Best Local Similarity 84.8%; Score 28; DB 4; Length 7;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPyXL 8
Db 1 PRPyYL 7

RESULT 12

US-09-484-318-7
; Sequence 7, Application US/09484318

Patient No. 6180085
; GENERAL INFORMATION:

APPLICANT: Achillefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Dorshow, Richard B

APPLICANT: Bugaj, Joseph E.
TITLE OF INVENTION: NOVEL DYES
FILE REFERENCE: DNA STRING

CURRENT APPLICATION NUMBER: US/09/484,318
CURRENT FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7
LENGTH: 8

TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
NAME/KEY: SITE

LOCATION: (1)
OTHER INFORMATION: THIS IS D-LYSINE.

OTHER INFORMATION: Description of Artificial Sequence:ANALOG OF
OTHER INFORMATION: NEUROTENSIN

US-09-484-318-7

Query Match
Best Local Similarity 84.8%; Score 28; DB 3; Length 8;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPyXL 8
Db 1 PRPyYL 8

RESULT 13

US-09-484-319-7

; Sequence 7, Application US/09484319

; Patent No. 6180086

; GENERAL INFORMATION:
; APPLICANT: Achillefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NEW HYDROPHILIC CYANINE DYSES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,319
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: THIS IS D-LYSINE.
; OTHER INFORMATION: Description of Artificial Sequence:ANALOG OF
; OTHER INFORMATION: NEUROTENSIN
; OTHER INFORMATION: US-09-484-319-7

Query Match
Best Local Similarity 84.8%; Score 28; DB 3; Length 8;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPyXL 8
Db 1 PRPyYL 8

RESULT 14

US-09-484-320-7

; Sequence 7, Application US/09484320

; Patient No. 6180087
; GENERAL INFORMATION:

APPLICANT: Achillefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Dorshow, Richard B

APPLICANT: Bugaj, Joseph E.
TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
FILE REFERENCE: drafting
CURRENT APPLICATION NUMBER: US/09/484,320
CURRENT FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
NAME/KEY: SITE

LOCATION: (1)
OTHER INFORMATION: THIS IS D-LYSINE.
OTHER INFORMATION: Description of Artificial Sequence:ANALOG OF
OTHER INFORMATION: NEUROTENSIN

US-09-484-320-7

Query Match
Best Local Similarity 84.8%; Score 28; DB 3; Length 8;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPyXL 8
Db 1 PRPyYL 8

RESULT 15

US-09-484-321-7

; Sequence 7, Application US/09484321

; Patent No. 6183726
; GENERAL INFORMATION:

Query Match 84.8%; Score 28; DB 3; Length 8;
 Best Local Similarity 71.4%; Pred. No. 4.1e+05;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 2 PRRPyIL 8

RESULT 16
 US-09-484-323-7
 ; Sequence 7, Application US/09484323
 ; Patent No. 619041
 ; GENERAL INFORMATION:
 ; APPLICANT: Achilefu, Samuel
 ; APPLICANT: Rajagopalan, Raghavan
 ; APPLICANT: Dorshow, Richard B
 ; APPLICANT: Bugaj, Joseph E.
 ; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
 ; FILE REFERENCE: DNA STRING
 ; CURRENT APPLICATION NUMBER: US/09/484,323
 ; CURRENT FILING DATE: 2000-01-18
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 8
 ; TYPE: PRT
 ; FEATURE: SITE
 ; NAME/KEY: SITE
 ; LOCATION: (1)
 ; OTHER INFORMATION: THIS IS D-LYSINE.
 ; OTHER INFORMATION: Description of Artificial Sequence:ANALOG OF
 ; US-09-484-323-7

Query Match 84.8%; Score 28; DB 3; Length 8;
 Best Local Similarity 71.4%; Pred. No. 4.1e+05;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 2 PRRPyIL 8

RESULT 17
 US-09-484-323-7
 ; Sequence 7, Application US/09484323
 ; Patent No. 619041
 ; GENERAL INFORMATION:
 ; APPLICANT: Achilefu, Samuel
 ; APPLICANT: Rajagopalan, Raghavan
 ; APPLICANT: Dorshow, Richard B
 ; APPLICANT: Bugaj, Joseph E.
 ; TITLE OF INVENTION: NOVEL CYANINE AND INDOCYANINE DYE BIOCONJUGATES FOR
 ; FILE REFERENCE: 1668-286
 ; CURRENT APPLICATION NUMBER: US/09/325,769
 ; CURRENT FILING DATE: 1999-06-04
 ; EARLIER APPLICATION NUMBER: AITY DOCKET 1668-284
 ; EARLIER FILING DATE: 1999-05-20
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 8
 ; TYPE: PRT
 ; FEATURE: SITE
 ; NAME/KEY: SITE
 ; LOCATION: (1)
 ; OTHER INFORMATION: This is D-lysine.
 ; FEATUR
 ; OTHER INFORMATION: Description of Artificial Sequence:Analog of
 ; US-09-325-769-8

Query Match 84.8%; Score 28; DB 3; Length 8;
 Best Local Similarity 71.4%; Pred. No. 4.1e+05;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 2 PRRPyIL 8

RESULT 18
 US-09-636-170-7
 ; Sequence 7, Application US/09636170
 ; Patent No. 6266919
 ; GENERAL INFORMATION:
 ; APPLICANT: Achilefu, Samuel
 ; APPLICANT: Rajagopalan, Raghavan
 ; APPLICANT: Dorshow, Richard B
 ; APPLICANT: Bugaj, Joseph E.
 ; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
 ; FILE REFERENCE: DNA STRING
 ; CURRENT APPLICATION NUMBER: US/09/636,170
 ; CURRENT FILING DATE: 2000-08-10
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (1)
 ; OTHER INFORMATION: THIS IS D-LYSINE.
 ; OTHER INFORMATION: Description of Artificial Sequence:ANALOG OF
 ; US-09-484-323-7

Query Match 84.8%; Score 28; DB 3; Length 8;
 Best Local Similarity 71.4%; Pred. No. 4.1e+05;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 2 PRRPyIL 8

RESULT 19
 US-09-637-518-7
 ; Sequence 7, Application US/09637518

RESULT 21
US-09-863-971A-8
; Sequence 8, Application US/09863971A
; Patent No. 6641798
; GENERAL INFORMATION:
; APPLICANT: Achillefu, Samuel I.
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorschow, Richard B.
; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
; FILE REFERENCE: dnrstrng
; CURRENT APPLICATION NUMBER: US/09/637,518
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: THIS IS D-LYSINE.
OTHER INFORMATION: Description of Artificial Sequence:ANALOG OF
US-09-637-518-7

Query Match 84.8%; Score 28; DB 3; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Other Information: NEUROTENSIN

Qy 2 PXRPYXL 8
Db 2 PRRPYIL 8

RESULT 20
US-09-528-200-178
; Sequence 178, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: Licha, Kai
; APPLICANT: Becker, Andreas
; APPLICANT: Semmler, Wolfhard
; APPLICANT: Weidemann, Bertram
; APPLICANT: Hessnitus, Cartsen
; APPLICANT: Volkmer-Engert, Rudolf
; APPLICANT: Schneidner-Mergener, Jens
; APPLICANT: Bhargava, Sarah
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; TITLE OF INVENTION: FOR OPTICAL DIAGNOSIS
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; CURRENT FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 178
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-528-200-178

Query Match 84.8%; Score 28; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 0; Other Information: peptide

Qy 2 PXRPYXL 8
Db 2 PRRPYIL 8

RESULT 21
US-09-863-971A-8
; Sequence 8, Application US/09863971A
; Patent No. 6641798
; GENERAL INFORMATION:
; APPLICANT: Achillefu, Samuel I.
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorschow, Richard B.
; APPLICANT: Bugaj, Joseph E.
; APPLICANT: Mallinckrodt Inc.
; TITLE OF INVENTION: Tumor-Targeted Optical Contrast Agents
; FILE REFERENCE: MRD-65
; CURRENT APPLICATION NUMBER: US/09/863,971A
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/484,320
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: Xaa at location 1 represents D-Lys. Artificial sequence is completely synthesized.
US-09-863-971A-8

Qy 2 PXRPYXL 8
Db 2 PRRPYIL 8

RESULT 22
US-09-864-011A-8
; Sequence 8, Application US/09864011A
; Patent No. 6706254
; GENERAL INFORMATION:
; APPLICANT: Achillefu, Samuel I.
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorschow, Richard B.
; APPLICANT: Bugaj, Joseph E.
; APPLICANT: Mallinckrodt Inc.
; TITLE OF INVENTION: Receptor-Avid Exogenous Optical Contrast and Therapeutic
; TITLE OF INVENTION: Agents
; FILE REFERENCE: MRD-64
; CURRENT APPLICATION NUMBER: US/09/864,011A
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/484,322
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)..(8)
OTHER INFORMATION: Xaa at location 1 represents D-Lys. Artificial sequence is completely synthesized.
US-09-864-011A-8

Query Match 84.8%; Score 28; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 0; Other Information: peptide

Qy 2 PXRPYXL 8
Db 2 PRRPYIL 8

Db 2 | ||| | PRRPYIL 8

RESULT 23
US-09-978-725A-8
Sequence 8, Application US/09978725A
PATENT No. 6761878
GENERAL INFORMATION:
APPLICANT: Achilefu, Samuel I.
APPLICANT: Dorshow, Richard B.
APPLICANT: Rajagopal, Raghavan
APPLICANT: Bugaj, Joseph E.
APPLICANT: Mallinckrodt Inc.
TITLE OF INVENTION: Pathological Tissue Detection and Treatment Employing
FILE REFERENCE: MRD-73
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)...(8)
OTHER INFORMATION: Xaa at location 1 represents D-Lys. Artificial sequence is
OTHER INFORMATION: completely synthesized.
US-09-978-725A-8

Query Match 84.8%; Score 28; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPyXL 8
Db 2 PRRPYIL 8

RESULT 24
US-09-528-200-177
Sequence 177, Application US/09528200
Patent No. 6630570
GENERAL INFORMATION:
APPLICANT: LICHA, KAI
APPLICANT: BECKER, ANDREAS
APPLICANT: WIDENMANN, BERTJAM
APPLICANT: HESSNITS, CARTSEN
APPLICANT: VOLKMER-ENGERT, RUDOLF
APPLICANT: SCHNEIDER-MERGENER, JENS
APPLICANT: BHARGAVA, SARAH
TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
FILE REFERENCE: SCH-1731
CURRENT FILING DATE: 2000-03-17
PRIORITY FILING DATE: 1999-09-04
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 194
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-528-200-194

Query Match 84.8%; Score 28; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 8.9;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPyXL 8
Db 3 PRRPYIL 9

RESULT 26
US-08-141-344-6
Sequence 6, Application US/08141324
Patent No. 5475097
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Nadine
APPLICANT: Pike, Robert N.
TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
TITLE OF INVENTION: Protease
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

Query Match 84.8%; Score 28; DB 4; Length 9;
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-528-200-177

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; STRANDEDNESS: single
; TOPOLogy: linear
; MOLECULE TYPE: peptide
; HYPOThetical: NO
; MOLECULE TYPE: peptide
; TOPOLogy: linear
; LENGTH: 12 amino acids
; STRANDEDNESS: single
; HYPOTHICAL: NO

US-08-141-324-6

Query Match 84.8%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PXRPyXL 8
Db 6 PRRPyVL 12

RESULT 27
US-08-541-902-6
; Sequence 6, Application US/08541902
; Patent No. 5,707,620
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jen S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyrinomas gingivalis
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenline and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303

COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,902
; FILING DATE: 21-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid

Query Match 84.8%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PXRPyXL 8
Db 6 PRRPyVL 12

RESULT 28
US-09-202-832-4
; Sequence 4, Application US/09202832
; Patent No. 6,194,190
; GENERAL INFORMATION:
; APPLICANT: IZU, Yukiko
; APPLICANT: TANAKA, Tetsuki
; APPLICANT: MIYAGI, Masaru
; APPLICANT: TANIGAWA, Tetsuo
; APPLICANT: TOMONO, Jun
; APPLICANT: TSUNASAWA, Susumu
; APPLICANT: KATO, Ikuoshin
; TITLE OF INVENTION: NOVEL AMINO-TERMINAL DEBLOCKING ENZYME
; FILE REFERENCE: 1422-368P
; CURRENT APPLICATION NUMBER: US/09/202,332
; CURRENT FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xaa = N-pyroglutamyl-leucine
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Neurotensin
; OTHER INFORMATION: Manufactured by Peptide Institute, Inc.
; OTHER INFORMATION: manufactured by Peptide Institute, Inc.
US-09-202-832-4

Query Match 84.8%; Score 28; DB 3; Length 12;
Best Local Similarity 71.4%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PXRPyXL 8
Db 6 PRRPyVL 12

RESULT 29
US-07-714-540-8
; Sequence 8, Application US/07714540
; Patent No. 5,262,221
; GENERAL INFORMATION:
; APPLICANT: Almquist, Ronald G.
; APPLICANT: Toll, Lawrence
; TITLE OF INVENTION: ISOLATED ATRIAL PEPTIDE-DEGRADING
; TITLE OF INVENTION: ENZYME AND NOVEL COMPOUNDS USEFUL AS INHIBITORS THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Irrell & Manella
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/714,540
 FILING DATE: 1991-06-07
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Reed, Diane E.
 REGISTRATION NUMBER: 31-292
 REFERENCE/DOCKET NUMBER: 8500-0135.00
 TELEPHONE: 415-327-7250
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-714-540-8

Query Match 84.8%; Score 28; DB 1; Length 13;
 Best Local Similarity 71.4%; Pred. No. 12; Mismatches 5; Conservative 0; Indels 2; Gaps 0;
 Matches 5; Mismatches 0; Indels 2; Gaps 0;

QY 2 PXR~~P~~YL 8
 Db 7 PR~~R~~YL 13

RESULT 30
 US-08-428-488-11
 Sequence 117, Application US/08747137
 Patent No. 5945033

GENERAL INFORMATION:
 APPLICANT: BODOR, Nicholas S.
 TITLE OF INVENTION: BRAIN ENHANCED DELIVERY OF NEUROACTIVE PEPTIDES BY SEQUENTIAL METABOLISM
 NUMBER OF INVENTIONS: 1
 NUMBER OF SEQUENCES: 107
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Burns, Doane, Swecker & Mathis
 STREET: P.O. Box 1404
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: United States
 ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/747,137
 FILING DATE: 12-NOV-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/212,546
 FILING DATE: 14-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/069,831
 FILING DATE: 01-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/959,560
 FILING DATE: 13-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/641,720
 FILING DATE: 15-JAN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36-429
 REFERENCE/DOCKET NUMBER: 016197-000840US
 TELEPHONE: 415-576-0200
 INFORMATION FOR SEQ ID NO: 117:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 FEATURE: NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /product= "p-Glu"
 US-08-747-137-117

Query Match 84.8%; Score 28; DB 2; Length 13;

NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /product= "p-Glu"

Best Local Similarity 71.4%; Pred. No. 12; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 32
US-08-737-299A-1
; Sequence 1, Application US/08737299A
; Patent No. 5952664
GENERAL INFORMATION:
TITLE OF INVENTION: Labelled Peptide Compounds
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jeffrey S. Boone
STREET: 675 McDonnell Blvd.
CITY: St. Louis
STATE: MO
COUNTRY: US
ZIP: 63134
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,299
FILING DATE: 21-JUL-1997
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02131
FILING DATE: 21-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jeffrey S. Boone
REGISTRATION NUMBER: 29284
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1 (314) 654-8955
TELEFAX: 1 (314) 654-3156
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "PYROGLUTAMIC ACID"
US-08-737-299A-1
Query Match 84.8%; Score 28; DB 2; Length 13;
Best Local Similarity 71.4%; Pred. No. 12; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 33
US-09-334-254A-1
; Sequence 1, Application US/09334254A
; Patent No. 619436
GENERAL INFORMATION:
APPLICANT: MERTENS et al.
TITLE OF INVENTION: Labelled Peptide Compounds
NUMBER OF SEQUENCES: 7

RESULT 34
US-09-289-693-1
; Sequence 1, Application US/09289693
; Patent No. 6214790
GENERAL INFORMATION:
APPLICANT: Richelson, Elliott
APPLICANT: Cusack, Bernadette Marie
APPLICANT: Pang, Yuan-Ping
APPLICANT: McCormick, Daniel J.
APPLICANT: Faqu, Abdil
APPLICANT: Tyler, Bath Marie
APPLICANT: Boules, Mona
TITLE OF INVENTION: NEO-TRYPTOPHAN
FILE REFERENCE: 07039/141001
CURRENT APPLICATION NUMBER: US/09/289,693
CURRENT FILING DATE: 1999-04-09
EARLIER APPLICATION NUMBER: US 60/112,137
EARLIER FILING DATE: 1998-12-14
EARLIER APPLICATION NUMBER: US 60/098,119
EARLIER FILING DATE: 1998-08-27
EARLIER APPLICATION NUMBER: US 60/092,195
EARLIER FILING DATE: 1998-07-09
EARLIER APPLICATION NUMBER: US 60/081,356
EARLIER FILING DATE: 1998-04-10

NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa = pyrrolidone carboxylic acid
; US-09-289-693-1

Query Match 84.8%; Score 28; DB 3; Length 13;
Best Local Similarity 71.4%; Pred. No. 12; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPYXL 8
Db 7 PRRPYIL 13

RESULT 35
US-09-355-863-2
; Sequence 2, Application US/09355869
; Patent No. 631261
; GENERAL INFORMATION:
; TITLE OF INVENTION: METHOD FOR THE DETECTION AND LOCALIZATION OF MALIGNANT
; TUMOURS
; FILE REFERENCE: 168-304
; CURRENT APPLICATION NUMBER: US/09/355,869
; CURRENT FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/01964
; PRIOR FILING DATE: 1998-02-02
; PRIOR APPLICATION NUMBER: EP 97200297.6
; PRIOR FILING DATE: 1997-02-03
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; FEATURE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This site is pyroglutamate.
; US-09-355-869-2

Query Match 84.8%; Score 28; DB 3; Length 13;
Best Local Similarity 71.4%; Pred. No. 12; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXRPYXL 8
Db 7 PRRPYIL 13

RESULT 36
US-09-405-990-8
; Sequence 8, Application US/090605990
; Patent No. 634451
; GENERAL INFORMATION:
; APPLICANT: Craig, A. Grey
; APPLICANT: Griffen, David
; APPLICANT: Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Hillyard, David R.
; APPLICANT: Imperial, Junita
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Wagstaff, John D.
; APPLICANT: Layer, Richard T.
; APPLICANT: Jones, Robert M.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Salk Institute
; TITLE OF INVENTION: Conulakin-G, Analogs Thereof and Uses Therefor
; CURRENT APPLICATION NUMBER: US/09/420,797B
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/130,661
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 60/128,561
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/105,015
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Bos sp.

RESULT 37
US-09-420-797B-8
; Sequence 8, Application US/09420797B
; Patent No. 6362193
; GENERAL INFORMATION:
; APPLICANT: Craig, A. Grey
; APPLICANT: Griffen, David
; APPLICANT: Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Hillyard, David R.
; APPLICANT: Imperial, Junita
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Wagstaff, John D.
; APPLICANT: Layer, Richard T.
; APPLICANT: Jones, Robert M.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Salk Institute
; TITLE OF INVENTION: Conulakin-G, Analogs Thereof and Uses Therefor
; CURRENT APPLICATION NUMBER: US/09/420,797B
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/130,661
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 60/128,561
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/105,015
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Bos sp.

; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (1)
 ; OTHER INFORMATION: Xaa at residue 1 is pyro-Glu.
 US-09-420-797B-8
 Query Match 84.8%; Score 28; DB 3; Length 13;
 Best Local Similarity 71.4%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXRPyXL 8
 Db 7 PRRPyIL 13

RESULT 38
 US-09-605-991-8
 ; Sequence 8, Application US/09605991
 ; Patent No. 6489298
 GENERAL INFORMATION:
 ; APPLICANT: Craig, A. Grey
 ; APPLICANT: Griffen, David
 ; APPLICANT: Olivera, Baldomero M.
 ; APPLICANT: Watkins, Maren
 ; APPLICANT: Hilliard, David R.
 ; APPLICANT: Imperial, Juilta
 ; APPLICANT: Cruz, Lourdes J.
 ; APPLICANT: Wagstaff, John D.
 ; APPLICANT: Layer, Richard T.
 ; APPLICANT: McCabe, R. Tyler
 ; APPLICANT: Cognetix, Inc.
 ; APPLICANT: University of Utah Research Foundation
 ; TITLE OF INVENTION: Contulakin-G, Analogs Thereof and Uses Therefor
 ; FILE REFERENCE: Contulakin-G CIP
 ; CURRENT APPLICATION NUMBER: US/09/609,534
 ; CURRENT FILING DATE: 2000-06-30
 ; EARLIER APPLICATION NUMBER: US 60/130,661
 ; EARLIER FILING DATE: 1999-04-23
 ; EARLIER APPLICATION NUMBER: US 60/128,561
 ; EARLIER FILING DATE: 1999-04-09
 ; EARLIER APPLICATION NUMBER: US 60/105,015
 ; EARLIER FILING DATE: 1998-10-20
 ; EARLIER APPLICATION NUMBER: US 09/420,797
 ; EARLIER FILING DATE: 1999-10-19
 ; EARLIER APPLICATION NUMBER: US 09/
 ; EARLIER FILING DATE: 2000-06-29
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 8
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Bos sp.
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (1)
 ; OTHER INFORMATION: Xaa at residue 1 is pyro-Glu.
 US-09-609-534-8

RESULT 40
 US-09-528-200-10
 ; Sequence 10, Application US/00528200
 ; Patent No. 6630570
 ; GENERAL INFORMATION:
 ; APPLICANT: LICHA, KAI
 ; APPLICANT: BECKER, ANDREAS
 ; APPLICANT: SEMMLER, WOLFHARD
 ; APPLICANT: HESSNITS, CARTSEN
 ; APPLICANT: VOLMER-ENGERT, RUDOLF
 ; APPLICANT: SCHNEIDER-MERGNER, JENS
 ; APPLICANT: BHARGAVA, SARAH
 ; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
 ; FILE REFERENCE: SCH-1731
 ; CURRENT APPLICATION NUMBER: US/09/528,200
 ; CURRENT FILING DATE: 2000-03-17
 ; PRIOR APPLICATION NUMBER: DE 199 17 713.9
 ; PRIOR FILING DATE: 1999-09-04
 ; NUMBER OF SEQ ID NOS: 196
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 10
 ; LENGTH: 13
 ; TYPE: PRT

RESULT 39
 US-09-609-534-8
 ; Sequence 8, Application US/09609534
 ; Patent No. 6525021
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig, A. Grey

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: pGlu
US-09-528-200-10

Query Match 84.8%; Score 28; DB 4; Length 13;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PXAPYXL 8
| |||
Db 7 PRRPYIL 13

Search completed: March 28, 2005, 08:39:01
Job time : 46 secs

99	28	84.8	9	2	AAR71753	Aar71753 Neurotens	PR	16-JUN-1999;	99US-0139452P.
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ALIGNMENTS									
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AAG28479							PR	18-JUN-1999;	99US-0139452P.
ID AAG28479	standard; protein; 104 AA.						PR	18-JUN-1999;	99US-0139452P.
XX							PR	18-JUN-1999;	99US-0139452P.
AC AAG28479;							PR	18-JUN-1999;	99US-0139452P.
XX							PR	18-JUN-1999;	99US-0139452P.
DT 17-OCT-2000 (first entry)							PR	18-JUN-1999;	99US-0139452P.
XX							PR	18-JUN-1999;	99US-0139452P.
DE Zea mays protein fragment SEQ ID NO: 33711.							PR	18-JUN-1999;	99US-0139452P.
XX							PR	18-JUN-1999;	99US-0139452P.
KW Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.							PR	18-JUN-1999;	99US-0139452P.
XX							PR	18-JUN-1999;	99US-0139452P.
OS Zea mays subsp. mays.							PR	18-JUN-1999;	99US-0139452P.
PN EP1033405-A2.							PR	18-JUN-1999;	99US-0139452P.
XX							PR	18-JUN-1999;	99US-0139452P.
PD 06-SEP-2000.							PR	18-JUN-1999;	99US-0139452P.
XX							PR	18-JUN-1999;	99US-0139452P.
PF 25-FEB-2000; 2000EP-00301439.							PR	18-JUN-1999;	99US-0139452P.
PR 25-FEB-1999; 99US-0121825P.							PR	18-JUN-1999;	99US-0139452P.
PR 03-MAR-1999; 99US-0123180P.							PR	18-JUN-1999;	99US-0139452P.
PR 03-MAR-1999; 99US-0123548P.							PR	18-JUN-1999;	99US-0139452P.
PR 23-MAR-1999; 99US-0125788P.							PR	18-JUN-1999;	99US-0139452P.
PR 23-MAR-1999; 99US-0126264P.							PR	18-JUN-1999;	99US-0139452P.
PR 29-MAR-1999; 99US-0126785P.							PR	18-JUN-1999;	99US-0139452P.
PR 01-APR-1999; 99US-0127462P.							PR	18-JUN-1999;	99US-0139452P.
PR 06-APR-1999; 99US-0128234P.							PR	18-JUN-1999;	99US-0139452P.
PR 16-APR-1999; 99US-0129845P.							PR	18-JUN-1999;	99US-0139452P.
PR 19-APR-1999; 99US-0130077P.							PR	18-JUN-1999;	99US-0139452P.
PR 21-APR-1999; 99US-0130449P.							PR	18-JUN-1999;	99US-0139452P.
PR 23-APR-1999; 99US-0130510P.							PR	18-JUN-1999;	99US-0139452P.
PR 23-APR-1999; 99US-0130891P.							PR	18-JUN-1999;	99US-0139452P.
PR 30-APR-1999; 99US-013208P.							PR	18-JUN-1999;	99US-0139452P.
PR 30-APR-1999; 99US-0132407P.							PR	18-JUN-1999;	99US-0139452P.
PR 04-MAY-1999; 99US-0132484P.							PR	18-JUN-1999;	99US-0139452P.
PR 05-MAY-1999; 99US-0132485P.							PR	18-JUN-1999;	99US-0139452P.
PR 05-MAY-1999; 99US-0132486P.							PR	18-JUN-1999;	99US-0139452P.
PR 07-MAY-1999; 99US-013263P.							PR	18-JUN-1999;	99US-0139452P.
PR 11-MAY-1999; 99US-01334256P.							PR	18-JUN-1999;	99US-0139452P.
PR 14-MAY-1999; 99US-0134218P.							PR	18-JUN-1999;	99US-0139452P.
PR 14-MAY-1999; 99US-0134219P.							PR	18-JUN-1999;	99US-0139452P.
PR 14-MAY-1999; 99US-0134221P.							PR	18-JUN-1999;	99US-0139452P.
PR 14-MAY-1999; 99US-0134370P.							PR	18-JUN-1999;	99US-0139452P.
PR 18-MAY-1999; 99US-0134768P.							PR	18-JUN-1999;	99US-0139452P.
PR 19-MAY-1999; 99US-0134941P.							PR	18-JUN-1999;	99US-0139452P.
PR 20-MAY-1999; 99US-0135124P.							PR	18-JUN-1999;	99US-0139452P.
PR 21-MAY-1999; 99US-0135353P.							PR	18-JUN-1999;	99US-0139452P.
PR 24-MAY-1999; 99US-0135629P.							PR	18-JUN-1999;	99US-0139452P.
PR 25-MAY-1999; 99US-0136021P.							PR	18-JUN-1999;	99US-0139452P.
PR 27-MAY-1999; 99US-0136392P.							PR	18-JUN-1999;	99US-0139452P.
PR 10-JUN-1999; 99US-0138540P.							PR	18-JUN-1999;	99US-0139452P.
PR 01-JUN-1999; 99US-0138847P.							PR	18-JUN-1999;	99US-0139452P.
PR 03-JUN-1999; 99US-0137528P.							PR	18-JUN-1999;	99US-0139452P.
PR 04-JUN-1999; 99US-0137724P.							PR	18-JUN-1999;	99US-0139452P.
PR 08-JUN-1999; 99US-0138949P.							PR	18-JUN-1999;	99US-0139452P.
PR 20-MAY-1999; 99US-0138847P.							PR	18-JUN-1999;	99US-0139452P.
PR 14-JUN-1999; 99US-0139119P.							PR	18-JUN-1999;	99US-0139452P.
PR 16-JUN-1999; 99US-0139452P.							PR	18-JUN-1999;	99US-0139452P.

PR 13-AUG-1999; 990US-0148565P.
 PR 13-AUG-1999; 990US-0148684P.
 PR 16-AUG-1999; 990US-0149368P.
 PR 17-AUG-1999; 990US-0149175P.
 PR 18-AUG-1999; 990US-0149426P.
 PR 20-AUG-1999; 990US-0149722P.
 PR 20-AUG-1999; 990US-0149723P.
 PR 20-AUG-1999; 990US-0149929P.
 PR 21-AUG-1999; 990US-0149902P.
 PR 23-AUG-1999; 990US-014999P.
 PR 23-AUG-1999; 990US-0150566P.
 PR 23-AUG-1999; 990US-0151303P.
 PR 31-AUG-1999; 990US-0151438P.
 PR 27-AUG-1999; 990US-0151065P.
 PR 27-AUG-1999; 990US-0151066P.
 PR 30-AUG-1999; 990US-0151080P.
 PR 30-AUG-1999; 990US-0151930P.
 PR 01-SEP-1999; 990US-0151930P.
 PR 07-SEP-1999; 990US-0152363P.
 PR 10-SEP-1999; 990US-0153070P.
 PR 13-SEP-1999; 990US-0153758P.
 PR 15-SEP-1999; 990US-0154018P.
 PR 16-SEP-1999; 990US-0154039P.
 PR 20-SEP-1999; 990US-0154779P.
 PR 22-SEP-1999; 990US-0155139P.
 PR 23-SEP-1999; 990US-0155486P.
 PR 24-SEP-1999; 990US-0155659P.
 PR 28-SEP-1999; 990US-015665P.
 PR 29-SEP-1999; 990US-0156596P.
 PR 04-OCT-1999; 990US-0157117P.
 PR 05-OCT-1999; 990US-0157753P.
 PR 06-OCT-1999; 990US-0157865P.
 PR 07-OCT-1999; 990US-0158029P.
 PR 08-OCT-1999; 990US-0158232P.
 PR 12-OCT-1999; 990US-0158369P.
 PR 13-OCT-1999; 990US-0159293P.
 PR 13-OCT-1999; 990US-0159294P.
 PR 13-OCT-1999; 990US-0159295P.
 PR 14-OCT-1999; 990US-0159329P.
 PR 14-OCT-1999; 990US-0159330P.
 PR 14-OCT-1999; 990US-0159331P.
 PR 14-OCT-1999; 990US-0159637P.
 PR 14-OCT-1999; 990US-0159638P.
 PR 18-OCT-1999; 990US-0159584P.
 PR 21-OCT-1999; 990US-0160741P.
 PR 21-OCT-1999; 990US-0160767P.
 PR 21-OCT-1999; 990US-0160768P.
 PR 21-OCT-1999; 990US-0160770P.
 PR 21-OCT-1999; 990US-0160814P.
 PR 21-OCT-1999; 990US-0160815P.
 PR 22-OCT-1999; 990US-0160980P.
 PR 22-OCT-1999; 990US-0160981P.
 PR 22-OCT-1999; 990US-0160989P.
 PR 25-OCT-1999; 990US-0161404P.
 PR 25-OCT-1999; 990US-0161405P.
 PR 25-OCT-1999; 990US-0161406P.
 PR 26-OCT-1999; 990US-0161359P.
 PR 26-OCT-1999; 990US-0161360P.
 PR 26-OCT-1999; 990US-0161361P.
 PR 28-OCT-1999; 990US-0161920P.
 PR 28-OCT-1999; 990US-0161992P.
 PR 28-OCT-1999; 990US-0161993P.
 PR 29-OCT-1999; 990US-0162142P.

Query Match 90.9%; Score 30; DB 3; Length 104;
 Best Local Similarity 71.4%; Pred. No. 1.3e-02; Mismatches 2; Indels 0; Gaps 0;

RESULT 2
 AAB31540 ID AAB31540 standard; peptide; 8 AA.
 XX AC AAB31540;
 XX DT 20-APR-2001 (first entry)
 XX DE Amino acid sequence of a peptide analogue of neurotensin.
 XX KW Neurotensin; neurotensin receptor; neurotensin analogue; tumour;
 KW small cell lung carcinoma; exocrine pancreatic cancer; Ewing sarcoma;
 KW meningioma; medulloblastoma; astrocytoma.
 OS Synthetic.

FH Key difference Location/Qualifiers

FT FT Misc-difference 1 /note= "D-form residue"
 FT FT Modified-site 1 /note= "Diethylenetriamine pentaacetic acid (DTPA)"
 FT FT Modified-site 2 /note= "attached"
 FT FT Modified-site 3 /note= "(N-amidinopiperidinyl) homoolanine or (N-amidinopiperidinyl) homoalanine"
 FT FT Modified-site 4 /note= "t-butylglycine"
 FT FT Modified-site 5 /note= "-OH attached"
 FT FT Modified-site 6 /note= "-OH attached"
 XX PN WO200078796-A2.
 XX PR 24-JUN-1999; 990US-0140913P.
 XX PR 21-JUN-2000; 2000US-0213068P.
 XX PA (MILCOW) MALLINCKRODT INC.
 XX PA (SRIN/) SRINTVANAN A.
 XX PA (ERIO/) ERION J L.
 PA (SCHE/) SCHMIDT M A.
 XX PI Srinivasan A, Erion JL, Schmidt MA;
 XX DR WPI; 2001-102696/11.
 XX PT Novel neurotensin peptides for diagnosing and treating tumors such as
 PT small cell lung carcinomas, contain arginine mimics.
 XX PS Claim 14; Page 33; 39pp; English.

CC The present sequence represents a peptide analogue of neurotensin.
 CC Neurotensin (see AAB31521) is a small peptide which is isolated from
 CC bovine hypothalamus. High concentrations of neurotensin receptors are
 CC found in several tumour cells. However, neurotensin has a short half-life.
 CC The neurotensin analogues of the invention contain arginine mimics,
 CC which results in increased serum stability and stability. The neurotensin
 CC analogues have selective affinity for neurotensin receptors. The peptide
 CC analogues are also resistant to enzymatic degradation. The IC50 value of
 CC the neurotensin analogue is comparable to native neurotensin. Neurotensin
 CC analogues are used for diagnosis and treatment of tumors, such as small
 CC cell lung carcinoma, exocrine pancreatic cancer, Ewing sarcoma,
 CC meningioma, medulloblastoma or astrocytoma by administering the peptide
 CC sequence 8 AA;

SQ Sequence 8 AA;

Query Match 87.9%; Score 29; DB 4; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06; Mismatches 6; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
 Db 8 PARPySL 14

PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 03-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 03-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-023363P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
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 PR 02-OCT-2000; 2000US-0236370P.
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 PR 02-OCT-2000; 2000US-0237039P.
 PR 13-OCT-2000; 2000US-0237040P.
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 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
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 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0244647P.
 PR 08-NOV-2000; 2000US-02446475P.
 PR 08-NOV-2000; 2000US-02446476P.
 PR 08-NOV-2000; 2000US-02446477P.
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 PR 08-NOV-2000; 2000US-02446524P.
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 PR 08-NOV-2000; 2000US-02446526P.
 PR 08-NOV-2000; 2000US-02446527P.
 PR 17-NOV-2000; 2000US-02446528P.
 PR 08-NOV-2000; 2000US-02446532P.
 PR 08-NOV-2000; 2000US-02446609P.
 PR 08-NOV-2000; 2000US-02446610P.
 PR 08-NOV-2000; 2000US-02446611P.
 PR 08-NOV-2000; 2000US-02446613P.
 PR 17-NOV-2000; 2000US-02449207P.
 PR 17-NOV-2000; 2000US-02449212P.
 PR 17-NOV-2000; 2000US-02449213P.
 PR 17-NOV-2000; 2000US-02449214P.
 PR 17-NOV-2000; 2000US-02449215P.
 PR 17-NOV-2000; 2000US-02449216P.
 PR 17-NOV-2000; 2000US-0249217P.

PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249246P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-025091P.
 PR 03-DEC-2000; 2000US-0251030P.
 PR 03-DEC-2000; 2000US-0251980P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 05-DEC-2000; 2000US-0251477P.
 PR 08-DEC-2000; 2000US-0251850P.
 PR 08-DEC-2000; 2000US-025160P.
 PR 08-DEC-2000; 2000US-0251860P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254090P.
 PR 05-JAN-2001; 2001US-0259670P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-49342652.
 DR N-PSDB; AAK60781.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
 PS Claim 11; SEQ ID NO 15593; 3071pp + Sequence listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/hematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 CC to AAK87694 represent human immune/hematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK54950 and AAM62169 CC represent sequences used in the exemplification of the present invention XX Sequence 53 AA;

Query Match 87.9%; Score 29; DB 4; Length 53;
 Best Local Similarity 85.7%; Pred. No. 1e02; Mismatches 1; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	2 PXRDXYL 8
DB	44 PXRPSYL 50

RESULT 5
 AAU67965
 ID AAU67965 standard; protein; 70 AA.
 XX
 AC AAU67965;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #28861.
 XX

KW SAPHO syndrome; synovitis; acne; pustulosis; hypertrichosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX Propionibacterium acnes.
 XX WO200181581-A2.
 PN
 XX 01-NOV-2001.
 XX PF 20-APR-2001; 2001WO-US012865.
 XX PR 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-0208841P.
 PR 07-JUL-2000; 2000US-0216747P.
 XX PA (CORI-) CORIXA CORP.
 XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PT L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX DR WPI; 2001-616774/71.
 DR N-PSDB; AAS55773.
 XX PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX PS Example 1; SEQ ID NO 29160; 1069pp; English.
 XX CC Sequences AAU39105-AAU8017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertrichosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes protein. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 70 AA;

Query Match	87.9%	Score	29	DB	4	Length	70
Best Local Similarity	71.4%	Pred. No.	1.4e+02				
Matches	5	Conservative	0	Mismatches	2	Indels	0
Gaps	0						

QY 2 PXRPYXL 8
 Db 38 PYRPySL 44

RESULT 6
 ABM64484 ABM64484 standard; protein; 70 AA.
 XX AC
 XX DT 20-OCT-2003 (first entry)
 XX DE Propionibacterium acnes predicted ORF-encoded polypeptide #29160.
 XX

KW Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.
 XX OS Propionibacterium acnes.
 XX PN WO2003133515-A1.
 XX PR 24-APR-2003.
 XX PD 11-OCT-2002; 2002WO-US032727.
 XX PR 15-OCT-2001; 2001US-00978825.
 XX PA (CORI-) CORIXA CORP.
 XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Valliee-Douglas J;
 XX DR WPI; 2003-381789/36.
 DR N-PSDB; ACF64702.
 XX PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX PS Example 1; SEQ ID NO 29160; 1481pp; English.
 XX CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM3524-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides; antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 70 AA;

Query Match	87.9%	Score	29	DB	6	Length	70
Best Local Similarity	71.4%	Pred. No.	1.4e+02				
Matches	5	Conservative	0	Mismatches	2	Indels	0
Gaps	0						

QY 2 PXRPYXL 8
 Db 38 PYRPySL 44

RESULT 7
 AAU65129
 ID AAU65129 standard; protein; 74 AA.
 XX AC AAU65129;
 XX

DT 27-FEB-2002 (first entry)
 XX DE Propionibacterium acnes immunogenic protein #26025.
 XX ID SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 OS Propionibacterium acnes.
 XX PN WO2001B1581-A2.
 XX PD 01-NOV-2001.
 XX PR 20-APR-2001; 2001WO-US012865.
 XX PR 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-0208841P.
 PR 07-JUL-2000; 2000US-0216747P.
 PA (CORI-) CORIXA CORP.
 XX PI Sheiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 DR XX WPI; 2001-616774/71.
 DR N-PSDB; AAS59660.

PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX Example 1; SEQ ID NO 26324; 1069pp; English.

CC Sequences AAU39105-AAU8017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis;
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptide and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 74 AA;

Query Match 87.9%; Score 29; DB 4; Length 74;
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPYXL 8
 ID |||||
 DB 38 PYRPySL 44

RESULT 8 ABM61648
 ID ABM61648 standard; protein; 74 AA.
 XX AC ABM61648;
 XX

DT 20-OCT-2003 (first entry)
 XX DE Propionibacterium acnes predicted ORF-encoded polypeptide #26324.
 XX Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
 KW immunosimulant; immune response; vaccine.
 OS Propionibacterium acnes.
 XX PN WO2003033515-A1.
 XX PD 24-APR-2003.
 XX PR 11-OCT-2002; 2002WO-US032727.
 XX PR 15-OCT-2001; 2001US-00978825.
 XX PA (CORI-) CORIXA CORP.
 XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Iodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallieve-Douglas J;
 XX DR N-PSDB; ACPF64589.
 XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX PS Example 1; SEQ ID NO 26324; 1481pp; English.

CC The invention relates to an isolated polynucleotide (ACFP4435-ACFP64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM4536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 74 AA;

Query Match 87.9%; Score 29; DB 6; Length 74;
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPYXL 8
 DB |||||
 DB 38 PYRPySL 44

RESULT 9 ADA54863

ID ADA54863 Standard; protein; 157 AA.
 XX
 AC ADA54863;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DB Human protein, SEQ ID 2431.
 XX
 KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
 KW inflammatory disease; osteoporosis; neurological disease.
 XX
 OS Homo sapiens.
 XX
 PT EP1293569-A2.
 XX
 PD 19-MAR-2003.
 XX
 PF 21-MAR-2002; 2002EP-00006586.
 XX
 PR 14-SEP-2001; 2001JP-00328381.
 PR 24-JAN-2002; 2002US-0350435P.
 XX
 PA (REB1-) HELIX RES INST.
 PA (REB1-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Iogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;
 DR WPI; 2003-395539/38.
 DR N-PSDB; ADA53224.
 XX
 PT New polynucleotides encoding full-length polypeptides, e.g. secretory or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
 XX
 PS Claim 14; SEQ ID NO 2431; 205pp; English.
 XX
 CC The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA5433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
 XX
 SQ Sequence 157 AA;

Query	2 PXRPyXL 8
Db	43 PNRPyTL 49

Query Match 87.9%; Score 29; DB 6; Length 157;
 Best Local Similarity 71.4%; Pred. No. 3.3e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 11
 ADG19768
 ID ADG19768 Standard; protein; 216 AA.
 XX
 AC ADG19768;
 XX
 DT 26-FEB-2004 (first entry)

G-Protein coupled receptor domain related consensus seq id 106.

DE G-protein coupled receptor domain related consensus seq id 106.

XX
 KW cytosolic; nephrotropic; antiinflammatory; cardiotropic; respiratory; gastrointestinal; neuroprotective; angiogenesis stimulator; gene therapy; 18336; 2466; 43238; 1983; 52881; 2391; 43449; 50289; 52872; 26908; cellular proliferative disorder; brain disorder; renal disorder; kidney disorder; inflammatory disorder; cardiovascular disorder; liver disorder; intestinal disorder; respiratory disorder; angiogenic disorder; human; G protein coupled receptor; GPCR; protein domain.
 KW Unidentified.

OS Unidentified.

XX
 PT US2003215860-A1.
 XX
 PD 20-NOV-2003.

XX
 PT 03-APR-2003; 2003US-00407079.
 XX
 PR 29-FEB-2000; 2000US-0186059P.
 PR 24-MAR-2000; 2000US-0191845P.
 PR 22-MAY-2000; 2000US-0206015P.
 PR 17-NOV-2000; 2000US-00715790.
 PR 28-FEB-2001; 2001US-00796138.
 PR 22-MAY-2001; 2001US-00863200.
 PR 22-AUG-2001; 2001US-0314041P.
 PR 22-AUG-2001; 2001US-0314185P.
 PR 21-AUG-2002; 2002US-00225034.
 PR 22-AUG-2002; 2002US-00226102.

PR 15-OCT-2002; 2002US-00372417.
 PR 29-OCT-2002; 2002US-00282837.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PT Glucksmann MA, Silos-Santiago I, Carroll JM, Galvin KM,
 XX
 DR WPI; 2004-010777/01.

XX
 PT New nucleic acid or polypeptide 18636, 2466, 43238, 1983, 52881, 2398,
 PT 45449, 50289, 52872 or 26908, useful in preparing a composition for
 PT treating e.g., cellular proliferative, brain, kidney, inflammatory or
 PT angiogenic disorder.

XX
 PS Disclosure; SEQ ID NO 106; 163PP; English.

XX
 CC The invention describes a new isolated 18636, 2466, 43238, 1983, 52881,
 CC 2398, 45449, 50289, 52872 or 26908 nucleic acid molecule comprising: a
 CC sequence comprising 939-3489 bp or its fragment comprising at least 15
 CC nucleotides; a sequence encoding a polypeptide comprising a sequence
 CC having 223-852 amino acids, or its allelic variant or fragment comprising
 CC at least 15 contiguous amino acids; or a sequence that hybridizes with
 CC (1) under stringent conditions. The nucleic acid or polypeptide is useful
 CC in preparing a composition for treating a disorder characterized by
 CC aberrant 18636, 2466, 43238, 1983, 52881, 2398, 45449, 50289, 52872 or
 CC 26908 activity e.g., cellular proliferative, brain, renal, kidney,
 CC angiogenic disorder. This is the amino acid sequence of a human G-protein
 CC coupled receptor 32 (GPR32), polypeptide used in the characterisation of
 XX novel human G-protein coupled receptor 26908.

XX Sequence 216 AA;

Query Match 87.9%; Score 29; DB 8; Length 216;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRRYXL 8
 Db 191 PDRPYSL 197

RESULT 12
 ABU44862
 ID ABU44862 standard; protein; 281 AA.
 XX
 AC ABU44862;
 XX
 DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #30389.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS *Salmonella paratyphi*.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PR 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 05-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Travick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 PR 21-MAR-2001; 2001US-00815242.

DR WPI; 2003-029926/02.
 DR N-PSDB; ACA48732.
 XX
 PT New antisense nucleic acids useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 72786; 176PP; English.

XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences

XX Sequence 281 AA;

Query Match 87.9%; Score 29; DB 6; Length 281;
 Best Local Similarity 71.4%; Pred. No. 6e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRRYXL 8
 Db 33 PORPYTL 39

RESULT 13
 ABU26400
 ID ABU26400 standard; protein; 312 AA.
 XX
 AC ABU26400;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #11927.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS *Campylobacter jejuni*.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PR 21-MAR-2002; 2002WO-US009107.

PR 06-SEP-2001; 2001US-00948993.
 PR 23-OCT-2001; 2001US-0342923P.
 PR 03-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA0270.

XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 54324; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 antisense nucleic acid; (4) an antibody capable of specifically binding
 the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 proliferation or the activity of a gene in an operon required for
 proliferation; (7) identifying a compound that influences the activity of
 the gene product or that has an activity against a biological pathway;
 CC (8) required for proliferation, or that inhibits cellular proliferation or the biological
 CC pathway in which the test compound that inhibits proliferation of an
 CC or a gene on which the test compound that inhibits proliferation lies
 CC product is required for proliferation, or that the biological
 CC pathway in which the test compound that inhibits proliferation lies
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC http://wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 312 AA;

Query Match	Score	DB	Length
Best Local Similarity	87.9%	6	314
Matches	5	Conservative	0
Mismatches	0		2
Indels	0		0
Gap	0		0

QY 2 PXRPyXL 8
 Db 62 PQRRyTL 68

RESULT 15
 AAU35421
 ID AAU35421 standard; protein; 315 AA.
 AC AAU35421;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Haemophilus influenzae cellular proliferation protein #62.
 XX
 KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
 XX
 KW antibacterial; drug design.
 OS *Haemophilus influenzae*.
 XX
 PN WO2001070955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US009190.
 XX
 PR 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206849P.
 PR 26-MAY-2000; 2000US-0207727P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253629P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.

XX
 Neisseria gonorrhoeae.
 OS
 XX
 PN WO200279243-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 12-FEB-2002; 2002WO-1B002069.
 XX
 PR 12-FEB-2001; 2001GB-00003424.
 XX
 DR (CHIR-) CHIRON SPA.
 XX
 PT New protein from *Neisseria gonorrhoeae*, useful for the manufacture of a
 PT medicament for treating or preventing *N. gonorrhoeae* infection.
 XX
 PS Disclosure; Page 561; 815pp; English.
 XX
 The present invention relates to proteins from *Neisseria gonorrhoeae*.
 CC Also disclosed are the nucleic acid molecules encoding the proteins and
 CC antibodies that specifically bind to the proteins. The composition
 CC comprising the protein, nucleic acid or antibody is useful for the
 CC manufacture of a medicament for treating or preventing *N. gonorrhoeae*
 CC infection, this may be in the form of a vaccine or gene therapy.
 CC Sequences given in records ABP76736-ABP81046 represent nucleic acid
 CC molecules of the invention
 XX
 Sequence 314 AA;

Query Match	Score	DB	Length
Best Local Similarity	87.9%	6	314
Matches	5	Conservative	0
Mismatches	0		2
Indels	0		0
Gap	0		0

QY 2 PXRPyXL 8
 Db 62 PQRRyTL 68

RESULT 15
 AAU35421
 ID AAU35421 standard; protein; 315 AA.
 AC AAU35421;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Haemophilus influenzae cellular proliferation protein #62.
 XX
 KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
 XX
 KW antibacterial; drug design.
 OS *Haemophilus influenzae*.
 XX
 PN WO2001070955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US009190.
 XX
 PR 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206849P.
 PR 26-MAY-2000; 2000US-0207727P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253629P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.

RESULT 14
 ABP79282
 ID ABR79282 standard; protein; 314 AA.
 XX
 AC ABR79282;
 XX
 DT 07-MAR-2003 (first entry)
 XX
 DE N. gonorrhoeae amino acid sequence SEQ ID 5094.
 XX
 KW Antibacterial; infection; vaccine; gene therapy.

XX
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

XX DR WPI; 2001-611495/70;

DR N-PSDB; AAS5280.

XX PT New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids.

XX Example 3; SEQ ID NO 11014; 511pp; English.

The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX Sequence 315 AA;
SQ

Query Match 87.9%; Score 29; DB 4; Length 315;
Best Local Similarity 71.4%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
| | | |
66 PNRPyTL 72

Db

RESULT 16

ABU39640 ID ABU39640 standard; protein; 315 AA.

AC ABU39640;

CC DT 19-JUN-2003 (first entry)

DB Protein encoded by Prokaryotic essential gene #25167.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design..

XX OS *Pseudomonas putida*.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PR 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 05-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-0072851.

PR 06-MAR-2002; 2002US-0362699P.
XX PR (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Porphy RA, Xu HH;

DR WPI; 2003-023926/02.

N-PSDB; ACA43510.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

XX PT Claim 25; SEQ ID NO 67564; 176pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product; or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-regulated gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX Sequence 315 AA;

Query Match 87.9%; Score 29; DB 6; Length 315;
Best Local Similarity 71.4%; Pred. No. 6.7e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
| | | |
67 PRRPyTL 73

Db

RESULT 17

ABU0234 ID ABU0234 standard; protein; 315 AA.

AC ABU0234;

CC DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #15761.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design..

XX OS *Haemophilus influenzae*.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PR 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 05-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-0072851.

PR 06-MAR-2002; 2002US-0362699P.

PR 06-SEP-2001; 2001US-01948993.
 PR XX
 PR 25-OCT-2001; 2001US-0342923P.
 PR OS
 PR 08-FEB-2002; 2002US-00072851.
 PR PN
 PR XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-02926/02.
 DR N-PSDB; ACA3104.

XX
 PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 58158; 176pp; English.

XX
 CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation or the biological identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (8) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 315 AA;

Query Match Best Local Similarity 87.9%; Score 29; DB 6; Length 315; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
 DB 66 PNRPyTL 72

RESULT 19
 ID AAU36341
 ID AAU36341 standard; protein; 316 AA.
 AC AAU36341;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Pseudomonas aeruginosa cellular proliferation protein #331.
 KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.
 OS Pseudomonas aeruginosa.
 XX
 PN WO2001070955-A2.
 XX
 DD 27-SEP-2001.
 PR 21-MAR-2001; 2001WO-US009180.
 XX
 PR 21-MAR-2000; 2000US-019107P.
 PR 23-MAY-2000; 2000US-020684P.
 PR 26-MAY-2000; 2000US-020772P.
 PR 23-OCT-2000; 2000US-024257P.
 PR 27-NOV-2000; 2000US-025362P.
 PR 22-DEC-2000; 2000US-025793P.

RESULT 18
 ID AAE30458
 ID AAE30458 standard; protein; 315 AA.
 AC AAE30458;
 XX
 DT 24-FEB-2003 (first entry)
 XX
 DB *Haemophilus influenzae* acetyl coa carboxylase protein.
 XX
 KW Virulence; veterinary; infection; pneumonia; antimicrobial drug; vaccine;

PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELIT-) BLITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zykind JW;
 XX DR WPI; 2001-611495/70.
 PR N-PSDB; AAC54200.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.
 XX
 PS Example 3; SEQ ID NO 11934; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia
 CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
 CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from Wipo at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 316 AA;

Query Match 87.9%; Score 29; DB 4; Length 316;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXRPyXL 8
 DB 67 PKRPyTL 73

RESULT 20
 ABU38589
 ID ABU38589 standard; protein; 316 AA.
 XX
 AC ABU38589;
 XX DT 19-JUN-2003 (first entry)
 DB Protein encoded by Prokaryotic essential gene #24116.
 XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX OS Pseudomonas aeruginosa.
 XX PN WO200277183-A2.
 XX PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US09107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-0072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) BLITRA PHARM INC.
 XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykind JW;
 PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI; 2003-029261/02.
 PR N-PSDB; ACA42459.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 66513; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-regulated gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) providing a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus, S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from Wipo at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 316 AA;

Query Match 87.9%; Score 29; DB 6; Length 316;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXRPyXL 8
 DB 67 PKRPyTL 73

RESULT 21
 ABU39034
 ID ABU39034 standard; protein; 317 AA.
 XX
 AC ABU39034;
 XX DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #24561.
 XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX OS Pasteurella multocida.
 XX PN WO200277183-A2.
 XX PD 03-OCT-2002.

PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 05-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 03-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (BLT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 N-PSDB; ACA42904.

XX
 PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
 PT
 XX
 PS Claim 25; SEQ ID NO 66958; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 317 AA;

Query Match 87.9%; Score 29; DB 6; Length 317;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2	PXRPyXL 8
Db 68	PNRPyTL 74

RESULT 22

Query Match 87.9%; Score 29; DB 6; Length 317;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2	PXRPyXL 8
Db 69	PRRPyTL 75

XX
 AC ABU42211;
 XX DT 19-JUN-2003 (first entry)

DB Protein encoded by Prokaryotic essential gene #27738.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Pseudomonas syringae.
 XX
 PN WO20027183-A2.
 XX
 PR 03-OCT-2002.
 XX
 PA (BLT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (BLT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR N-PSDB; ACA46081.
 XX
 PS Claim 25; SEQ ID NO 70135; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 317 AA;

Query Match 87.9%; Score 29; DB 6; Length 317;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2	PXRPyXL 8
Db 69	PRRPyTL 75

RESULT 23
 AAU34455
 ID AAU34455 standard; protein; 319 AA.
 AC AAU34455;
 XX
 DT 14-FEB-2002 (first entry)
 DE E. coli cellular proliferation protein #36.
 KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.
 OS Escherichia coli.
 XX
 PN WO200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US009180.
 XX
 PR 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207727P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;
 PI Yamamoto RT, Xu HH;
 XX
 DR WPI; 2001-611495/70.
 XX
 PT New polynucleotides for the identification and development of
 antibiotics, comprise sequences of antisense nucleic acids.
 XX
 PS Example 3; SEQ ID NO 10048; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia
 CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note. The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 319 AA;

SQ Query Match 87.9%; Score 29; DB 4; Length 319;
 Best local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 70 PQRPTL 76

RESULT 24
 AAU38304
 ID AAU38304 standard; protein; 319 AA.
 AC AAU38304;
 XX
 DT 14-FEB-2002 (first entry)
 DE *Salmonella typhi* cellular proliferation protein #195.
 KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.
 OS *Salmonella typhi*.
 XX
 PN WO200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US009180.
 XX
 PR 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207727P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;
 PI Yamamoto RT, Xu HH;
 XX
 DR WPI; 2001-611495/70.
 XX
 PT New polynucleotides for the identification and development of
 antibiotics, comprise sequences of antisense nucleic acids.
 XX
 PS Example 3; SEQ ID NO 13897; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia
 CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note. The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 319 AA;

SQ Query Match 87.9%; Score 29; DB 4; Length 319;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PXRPyXL 8
 Db 70 PQRPTL 76

RESULT 25
 ABU27909 87.9%; Score 29; DB 6; Length 319;
 ID Best Local Similarity 71.4%; Pred. No. 6; +02;
 XX Matches 5; Conservative 0; Mismatches 2;
 AC Indels 0; Gaps 0;
 XX DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #13436.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX OS Enterobacter cloacae.
 XX PA 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 XX PN WO200277183-A2.
 XX PD 03-OCT-2002.
 XX PR 06-SEP-2001; 2001US-00548993.
 XX PR 05-OCT-2001; 2001US-0342923P.
 XX PR 08-FEB-2002; 2002US-00072851.
 XX PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI; 2003-029926/02.
 DR N-PSDB; ACA31779.

PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for rational drug discovery programs.
 PT isolate candidate molecules for rational drug discovery programs.
 XX Claim 25; SEQ ID NO 55833; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences Sequence 319 AA;

RESULT 26
 ABU48247 87.9%; Score 29; DB 6; Length 319;
 ID Best Local Similarity 71.4%; Pred. No. 6; +02;
 XX Matches 5; Conservative 0; Mismatches 2;
 AC Indels 0; Gaps 0;
 XX DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #33774.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 OS *Salmonella typhi*.
 XX PN WO200277183-A2.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 XX PR 06-SEP-2001; 2001US-00548993.
 XX PR 05-OCT-2001; 2001US-0342923P.
 XX PR 08-FEB-2002; 2002US-00072851.
 XX PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI; 2003-029926/02.
 DR N-PSDB; ACA32117.

PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for rational drug discovery programs.
 PT isolate candidate molecules for rational drug discovery programs.
 XX Claim 25; SEQ ID NO 76171; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for

CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences
 CC Sequence 319 AA;

Query Match 87.9%; Score 29; DB 6; Length 319;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 2;

QY 2 PXRPyXL 8
 Db 70 PQRPYL 76

RESULT 27

ABU37156
 ID ABU37156 standard; protein; 319 AA.

AC ABU37156;
 XX DT 23-OCT-2003 (revised)
 DT 19-JUN-2003 (first entry)

DB Protein encoded by Prokaryotic essential gene #22683.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
 KW
 OS Neisseria gonorrhoeae.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PR 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 05-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.

DR N-PADB; ACRA41026.

XX PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 65000; 1766PP; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to
 CC standardise OS Field)

CC Sequence 319 AA;

Query Match 87.9%; Score 29; DB 6; Length 319;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 2;

QY 2 PXRPyXL 8
 Db 67 PQRPYL 73

RESULT 28

ABU4948B
 ID ABU4948B standard; protein; 319 AA.

AC ABU4948B;
 XX DT 19-JUN-2003 (first entry)

DB Protein encoded by Prokaryotic essential gene #35015.

XX PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PD 03-OCT-2002.

XX PR 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PR Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PR Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.

DR N-PADB; ACRA53358.

XX PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 77412; 1766PP; English.

CC The invention relates to an isolated nucleic acid comprising any one of

CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits cellular proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences

XX Sequence 319 AA;

Query Match 87.9%; Score 29; DB 6; Length 319;
 Best local Similarity 71.4%; Pred. No. 6.8e-02; OS ABU31682
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXRPyXL 8
 Db 70 PRRPyTL 76

RESULT 29

Query Match 87.9%; Score 29; DB 6; Length 319;
 Best local Similarity 71.4%; Pred. No. 6.8e-02; OS ABU31682
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 AC ABU31682;
 XX DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #17209.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX Klebsiella pneumoniae.
 OS WO200277183-A2.

XX 21-MAR-2002; 2002WO-US009107.

PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00848993.

XX 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELTRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
 XX Yamamoto R, Forsyth RA, Xu HH;
 PI Wall D, Trawick JD, Carr GA;

DR WPI; 2003-029926/02.
 N-PSDB; ACA35552.

New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX PS claim 25; SEQ ID NO 59606; 176PP; English.

The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences

XX Sequence 319 AA;

Query Match 87.9%; Score 29; DB 6; Length 319;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02; OS ABU31682
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPyXL 8
 Db 70 PRRPyTL 76

RESULT 30

ID ABU40645 standard; protein; 319 AA.
 XX ABI40645;
 XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #26172.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 OS Proteus sp.
 XX WO200277183-A2.

XX 03-OCT-2002.
 PR 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.
 PR 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.
 PR 23-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-028926/02.
 N-ISDB; ACA4515.

XX
 PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 68669; 1766pp; English.

XX
 CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
 (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 319 AA;

Query Match Best local Similarity 87.9%; Score 29; DB 6; Length 319; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXRPyXL 8
 Db 70 PLRPyTL 76

RESULT 31
 ABU5047
 ID ABU50047 Standard; protein; 319 AA.
 AC ABU50047;
 XX DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #35574.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX
 OS *Versinia pestis*.
 XX WO200277183 A2.
 PN
 XX PD 03-OCT-2002.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
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 XX PR 21-MAR-2001; 2001US-00815242.
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 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
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 XX PR 21-MAR-2001; 2001US-00815242.
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 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
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 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
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 XX PA (ELIT-) ELITRA PHARM INC.
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 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
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 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
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 XX PR 21-MAR-2001; 2001US-00815242.
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 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
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 XX PR 21-MAR-2001; 2001US-00815242.
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 XX PA (ELIT-) ELITRA PHARM INC.
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 XX PR 21-MAR-2001; 2001US-00815242.
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 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
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 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
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 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
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 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
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 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
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 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
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 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
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 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
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 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
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 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
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 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
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 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00548993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.

ABU37970
ID ABU37970 standard; protein; 319 AA.
AC ABU37970;
XX
DT 19-JUN-2003 (first entry)
XX DB Protein encoded by Prokaryotic essential gene #23497.
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS *Neisseria meningitidis*.
XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX PP 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 22-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELTRA PHARM INC.
PA XX
PT Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW; Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH; DR WPI; 2003-0329926/02.
XX PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
PT
XX
PS Claim 25; SEQ ID NO 65894; 176pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation or an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

XX SQ Sequence 319 AA;

Query Match 87.9%; Score 29; DB 6; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.8e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	2 PXRPyXL 8
Db	67 PQRPyTL 73

RESULT 33
ABU47369
ID ABU47369 standard; protein; 319 AA.
AC ABU47369;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #32896.
XX PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELTRA PHARM INC.
PA XX
PT Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW; Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH; DR WPI; 2003-0329926/02.
XX PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
PS Claim 25; SEQ ID NO 7293; 176pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences
 XX SQ Sequence 319 AA;

RESULT 34
 ABU15268 ID ABU15268 standard; protein; 319 AA.
 XX AC ARU15268:
 XX DT 19-JUN-2003 (first entry)
 XX DE Protein encoded by Prokaryotic essential gene #795.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX OS Escherichia coli.
 XX PN WO200277183-A2.
 XX PD 03-OCT-2002.
 XX PF 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00848993.
 PR 22-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELI-T) ELTTRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI; 2003-029926/02.
 DR N-PSDB; ACCA9138.
 XX PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX PS Claim 25; SEQ ID NO 43192; 176pp; English.
 XX CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation or the biological
 CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) preparing a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences
 XX SQ Sequence 319 AA;

RESULT 35
 ADD15500 ID ADD15500 standard; protein; 319 AA.
 XX AC ADD15500;
 XX DT 15-JAN-2004 (first entry)
 XX DE Escherichia coli AccA protein (SeqID 65).
 KW microbial; antimicrobial; membrane biosynthesis; pathogenic;
 KW immunological response; vaccination; surface disinfectant;
 KW personal hygiene application; food preservative; enzyme; AccA;
 KW acetyl-CoA carboxylase carboxyl transferase subunit alpha.
 XX OS Escherichia coli.
 XX PN WO2003025007-A2.
 XX PD 27-MAR-2003.
 XX PF 20-SEP-2002; 2002WO-CA001428.
 XX PR 21-SEP-2001; 2001US-0323992P.
 PR 21-SEP-2001; 2001US-0324152P.
 PR 25-SEP-2001; 2001US-0324692P.
 PR 26-OCT-2001; 2001US-0339924P.
 PR 29-OCT-2001; 2001US-0350973P.
 PR 30-OCT-2001; 2001US-0340924P.
 PR 27-NOV-2001; 2001US-0333660P.
 PR 18-DEC-2001; 2001US-0341732P.
 PR 18-DEC-2001; 2001US-0341776P.
 PR 19-DEC-2001; 2001US-0341949P.
 XX PA (AFFI-) AFFINITY PHARM INC.
 XX PI Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B;
 PI Donagala M, Houston S, Kanagarajah D, Nethery K, Ng I, Mansouri K;
 PI McDonald M, Pinder B, Viola C, Wrezel O;
 XX DR WPI; 2003-46811944.
 DR N-PSDB; ADD15499.
 XX PT Novel crystallized recombinant polypeptides from *Staphylococcus aureus*,

PT Streptococcus pneumoniae and Escherichia coli and which are involved in PT membrane biosynthesis, useful as targets for pathogenic bacteria.

XX Claim 86; SEQ ID NO 65; 325pp; English.

CC This invention relates to the structural and functional characterisation CC of microbial polypeptides from *Staphylococcus aureus* (*S. aureus*), *Escherichia coli* (*E. coli*) CC and *Escherichia coli* (*E. coli*). Specifically, it refers to polypeptides that are involved in membrane biosynthesis, which play a critical role in the life cycle and viability of their pathogenic species CC of origin, and hence provide valuable drug targets. Furthermore, the invention describes modified version of these proteins that facilitate CC characterisation by labelling with isotopic or heavy atoms, and also information to aid the discovery of therapeutic molecules to treat CC disorders associated with a particular pathogenic species. As such, they are useful for inducing an immunological response in an individual and as an antigen for vaccination purposes. The polypeptides are also useful for developing antimicrobial agents for use as surface disinfectants, personal hygiene applications and as food preservatives or in treating food products to eliminate potential pathogens. This polypeptide sequence CC is the ACCA protein encoded by DNA predicted from the genomic sequence of CC *E. coli* acetyl-CoA carboxylase carboxyl transferase subunit alpha of the CC invention.

XX Sequence 319 AA;

Query Match 87.9%; Score 29; DB 7; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PXRPYXL 8
Db 70 PORPYTL 76

RESULT 36

XX ADD15502 standard; protein; 319 AA.

XX AC ADD15502;
XX DT 15-JAN-2004 (first entry) -
XX DE Escherichia coli AccA protein (SeqID 67).
XX KW microbial; antimicrobial; membrane biosynthesis; pathogenic;
KW immunological response; vaccination; surface disinfectant;
KW personal hygiene application; food preservative; enzyme; AccA;
KW acetyl-CoA carboxylase carboxyl transferase subunit alpha.
OS Escherichia coli.
XX PN WO2003025007-A2.
XX PD 27-MAR-2003.
XX PF 20-SEP-2002; 2002WO-CAO01428.
XX PR 21-SEP-2001; 2001US-0333992P.
PR 21-SEP-2001; 2001US-0324152P.
PR 25-SEP-2001; 2001US-0324692P.
PR 26-OCT-2001; 2001US-0339924P.
PR 29-OCT-2001; 2001US-0350973P.
PR 30-OCT-2001; 2001US-0340924P.
PR 27-NOV-2001; 2001US-0333666P.
PR 18-DEC-2001; 2001US-0341732P.
PR 18-DEC-2001; 2001US-0341776P.
PR 19-DEC-2001; 2001US-0341949P.
XX PA (AFPI-) AFFINITY PHARM INC.

PI Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B, Mansouri K; PT Donagai M, Houston S, Kanagarajah D, Nethery K, Ng I, McDonald M, Pinder B, Viola C, Wrezel O;
XX DR WPI; 2003-468119/44.
XX N-PSDB; ADD15501.

Query Match 87.9%; Score 29; DB 7; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PXRPYXL 8
Db 70 PORPYTL 76

RESULT 36

XX ADD15502 standard; protein; 319 AA.

XX AC ADD15502;
XX DT 15-JAN-2004 (first entry) -
XX DE Escherichia coli AccA protein (SeqID 67).
XX KW microbial; antimicrobial; membrane biosynthesis; pathogenic;
KW immunological response; vaccination; surface disinfectant;
KW personal hygiene application; food preservative; enzyme; AccA;
KW acetyl-CoA carboxylase carboxyl transferase subunit alpha.
OS Escherichia coli.
XX PN WO2003025007-A2.
XX PD 27-MAR-2003.
XX PF 20-SEP-2002; 2002WO-CAO01428.
XX PR 21-SEP-2001; 2001US-0333992P.
PR 21-SEP-2001; 2001US-0324152P.
PR 25-SEP-2001; 2001US-0324692P.
PR 26-OCT-2001; 2001US-0339924P.
PR 29-OCT-2001; 2001US-0350973P.
PR 30-OCT-2001; 2001US-0340924P.
PR 27-NOV-2001; 2001US-0333666P.
PR 18-DEC-2001; 2001US-0341732P.
PR 18-DEC-2001; 2001US-0341776P.
PR 19-DEC-2001; 2001US-0341949P.
XX PA (ELIT-) ELITRA PHARM INC.

PI Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B, Mansouri K; PT Donagai M, Houston S, Kanagarajah D, Nethery K, Ng I, McDonald M, Pinder B, Viola C, Wrezel O;
XX DR WPI; 2003-468119/44.
XX N-PSDB; ADD15501.

Query Match 87.9%; Score 29; DB 7; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PXRPYXL 8
Db 70 PORPYTL 76

RESULT 37

XX ABU40545 standard; protein; 320 AA.

XX ID ABU40545 standard; protein; 320 AA.
XX AC ABU40545;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #26072.
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Proteus sp.
XX PN WO200277183-A2.
XX PR 03-OCT-2002.
XX PD 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00848993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-0072851.
PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI; 2003-029926/02.
 DR N-PSDB; ACA4415.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 68469; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC brains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC parent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 320 AA;

Query Match 87.9%; Score 29; DB 6; Length 320;
 Best Local Similarity 71.4%; Pred. No. 6.9e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PXRPYXL 8
 | ||| |
 Db 71 PMRPyTL 77

RESULT 38

ID ABU23166
 XX ABU23166 standard; protein; 321 AA.

AC ABU23166;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #8693.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS *Bordetella pertussis*.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX XX

PF 21-MAR-2002; 2002MO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-0094933.
 PR 22-OCT-2001; 2001US-0342928P.
 PR 08-FEB-2002; 2002US-0072831.
 PR 06-MAR-2002; 2002US-0362693P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI; 2003-029926/02.
 DR N-PSDB; ACA27036.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 51090; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC parent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 321 AA;

Query Match 87.9%; Score 29; DB 6; Length 321;
 Best Local Similarity 71.4%; Pred. No. 6.9e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PXRPYXL 8
 | ||| |
 Db 67 PQRPYTL 73

RESULT 39

ID ABU22657
 XX ABU22657 standard; protein; 323 AA.

AC ABU22657;

XX DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #8184.
 XX KW Antisense; prokaryotic gene; cell proliferation; drug design.
 XX OS Burkholderia mallei.
 XX PN WO200277183-A2.
 XX PD 03-OCT-2002.
 XX PR 21-MAR-2002; 2002WO-US09107.
 XX PR 21-MAR-2001; 2001US-00815242.
 XX PR 06-SEP-2001; 2001US-0094893.
 XX PR 22-OCT-2001; 2001US-0342923P.
 XX PR 08-FEB-2002; 2002US-00072851.
 XX PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PS Claim 25; SEQ ID NO 50581; 1766pp; English.
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism's activity; (9) manufacturing an antibiotic; (10) profiling a
 CC compound; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus, S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 323 AA;

Query Match Score 29; DB 6; Length 323;
 Best Local Similarity 71.4%; Pred. No. 6.9e-02; Mismatches 5; Conservative 0; Indels 0; Gaps 0;
 Qy 2 PXRPXL 8
 Db 67 PQRPyTL 73

RESULT 40
 ABU1973
 ID ABU1973 standard; protein; 323 AA.
 XX AC ABU1973;
 XX DT 19-JUN-2003 (first entry)
 XX DE Protein encoded by Prokaryotic essential gene #5300.
 XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX OS Borrelia capacia.
 XX PN WO200277183-A2.
 XX PD 03-OCT-2002.
 XX PF 21-MAR-2002; 2002WO-US09107.
 XX PR 21-MAR-2001; 2001US-00815242.
 XX PR 06-SEP-2001; 2001US-00048993.
 XX PR 25-OCT-2001; 2001US-0342923P.
 XX PR 08-FEB-2002; 2002US-00072851.
 XX PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI; 2003-023926/02.
 XX PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 isolate candidate molecules for rational drug discovery programs.
 XX PS Claim 25; SEQ ID NO 47697; 1766pp; English.
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus, S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

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XX
SQ Sequence 323 AA;

Query Match 87.9%; Score 29; DB 6; Length 323;
Best Local Similarity 71.4%; Pred. No. 6.9e+02;
Matches 5; Conservative 0; Mismatches 2;
Indels 0; Gaps 0;

QY 2 PXRPyXL 8
| || |
67 PQRPYTL 73

Search completed: March 28, 2005, 08:35:06
Job time : 72 secs

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